PDB annotation		A, B; 9- CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE, 2 ENDOPEROXIDE	ä	ä		CTASE; OXIDOREDUCTASE ADR, NADPH: ADRENODOXIN OXIDOREDUCTASE; FLAVOENZYME, MAD ANALYSIS, F1 FCTRON TR ANSFER A SE		:: IR 15 KD
Coumpound	2CBA 4	PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9- MER; CHAIN: F;	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A;	ADRENODOXIN REDUCTASE; CHAIN: A;	SARCOSINE OXIDASE; CHAIN: A, B;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C O: FIMARATE
SEQFOL D score								
PMF score		-0.11	0.19	1.00	1.00	0.00	0.81	0.03
Verify score		0.06	-0.76	0.61	0.22	-0.65	0.31	-0.04
Psi Blast		0	3.4e-41	0	0	0.0045	6.8e-37	8.5e-53
END AA		089	241	714	089	82	430	437
STAR T AA		167	139	252	167	51	62	61
CHAI N ID		<b>∀</b>	A	၁	Y	A	A	V
PDB ID		lcvu	1d2v	1d2v	1diy	1cjc	1el5	1fum
SEQ ID NO:		1568	1568	1568	1568	1569	1569	1569

PDB annotation							The state of the s	OXIDOREDUCTASE FUMARATE REDUCTASE, SUCCINATE	DEHYDROGENASE, RESPIRATORY 2	CHAIN, CITRIC ACID CYCLE,	FLAVOPROTEIN, IRON-SULPHUR 3	PROTEIN, DIHAEM CYTOCHROME B		OXIDOREDUCTASE	OXIDOREDUCTASE						ACTIN-BINDING PROTEIN ACTIN-	BINDING PROTEIN, CALCIUM-	BINDING, PHOSPHORYLATION	ACTIN-BINDING PROTEIN ACTIN-	BINDING PROTEIN, CALCIUM-	BINDING, PHOSPHORYLATION	STRUCTURAL PROTEIN CALPONIN	HOMOLOGY, ACTIN BINDING,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN CALPONIN
Coumpound		HYDROPHOBIC PROTEIN; CHAIN: D, P;	OXIDOREDUCTASE DIHYDROLIPOAMIDE	DEHYDROGENASE (E.C.1.8.1.4)	COMPLEX WITH 1LPF 3	FLAVIN-ADENINE.	MINOCLEOI IDE (FAD) ILFF +	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT;	CHAIN: A, D; FUMARATE	REDUCTASE IRON-SULFUR	PROTEIN; CHAIN: B, E;	FUMARATE REDUCTASE	CYTOCHROME B SUBUNIT;	FLAVOCYTOCHROME C3	FUMARATE REDUCTASE:	CHAIN: A, D;	OXIDOREDUCTASE	DIHYDROLIPOAMIDE	DEHYDROGENASE (E.C.1.8.1.4)	SLAD 3	T-FIMBRIN; CHAIN; NULL;			T-FIMBRIN; CHAIN; NULL;			UTROPHIN; CHAIN: A, B;			UTROPHIN; CHAIN: A, B;
SEQFOL D score																								ţ			74.32			
PMF			20.0					0.04						-0.09			60.0				0.83			0.40						0.1
Verify			-0.23				700	-0.34						0.04			-0.09				09.0			0.54						0.84
Psi Blast			0.003				10.40	1.2e-43						8.5e-29			0.0015				5.1e-24			1.5e-29			4.5e-35		i	1.7e-34
END			82				207	437						434			83				230			230			232		000	232
STAR T AA			46					1 °						28			46				125			127			123		, 0,	126
CHAI			A					<b>V</b>						A			Ą										A			A
PDB ID			1lpf		-		121	Iqia						1908			3lad				Iaoa			laoa			1bhd		11.1.1	Iphd
SEQ ID	NO:		1569				15.00	1369						1569			1569				1571			1571			1571		1 2 77 1	12/1

A   127   232   4.56-35   0.85   1.00   UTROPHIN; CHAIN; A, B; B   126   235   8.56-43   8.6.88   SPECTRIN BETA CHAIN; CHAIN; CHAIN; A; B   127   235   8.56-43   0.86   1.00   SPECTRIN BETA CHAIN; CHAIN; A, B, C, CHAIN; CHAIN; CHAIN; CHAIN; CHAIN;	<u></u>	PDB ID	CHAI	STAR T AA	END	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN; A, B;           A         126         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN; A, B, C, CHAIN; A, B;           A         202         562         0         0.24         1.00         NUROPHIN ACTIN BINDING           A         212         564         0         0.24         1.00         BAZYME E2; CHAIN; B, B, C, C, UBIQUITIN-PROTEIN LIGASE           A         212         564         0         0.24         1.00         BAZYME E2; CHAIN; B, C,											HOMOLOGY ACTIN BINDING
A         127         232         4.5e-35         0.85         1.00         UTROPHIN; CHAIN; A, B;           A         126         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN: A, B, C, D, S           A         126         233         5.1e-35         0.68         1.00         UTROPHIN ACTIN BINDING           A         202         562         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE           A         212         564         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE           A         212         564         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE           BAA; CHARIS, A, B;         E3A; CHARIS, A, B;         E3A; CHARIS, A, B;         UBIQUITIN-PROTEIN LIGASE           A         212         564         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE           BAA; CHARIS, A, B;         E3A; CHARIS, A, B;         UBIQUITIN-PROTEIN LIGASE         UBIQUITIN-PROTEIN LIGASE											STRUCTURAL PROTEIN
A 126 235 8.5e-43	1bl	p	A	127	232	4.5e-35	0.85	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL, PROTEIN
A         127         235         8.5e-43         0.86         1.00         SPECTRIN BETA CHAIN;           A         126         233         1e-35         0.69         1.00         DYSTROPHIN; CHAIN: A, B, C, D;           A         126         233         5.1e-35         0.68         1.00         UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;           A         202         562         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE BASE CHAIN: A, B, C;           A         212         564         0         0.24         1.00         UBIQUITIN-PROTEIN LIGASE BASE CHAIN: B, C;           A         212         564         0         131.07         UBIQUITIN-PROTEIN LIGASE BASE CHAIN: A, B, C;           BASTYME E2; CHAIN: A, B, C;         UBIQUITIN-PROTEIN LIGASE BASE CHAIN: A, B, C;         UBIQUITIN-PROTEIN LIGASE BASE CHAIN: B, C;           A         115         207         1a.06         A	1bkr	<sub>8</sub>	<b>∀</b>	126	235	8.5e-43			86.88	SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
A 126 233 1e-35 0.69 1.00 DYSTROPHIN; CHAIN: A, B, C, D; D; CHAIN: A, B, C, D; CHAIN: A, B, C, D; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B; CHAIN: A, B, C; CHAIN: A, B, C; CHAIN: CHAIN: A, B, C; CHAIN:	16kr	a	Ą	127	235	8.5e-43	0.86	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CE) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
A 202 562 0 0.24 1.00 UTROPHIN ACTIN BINDING  A 202 562 0 0.24 1.00 UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; A 212 564 0 131.07 UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	<del>Q</del>	ង	∢	126	233	1e-35	0.69	1.00		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN
A 202 562 0 0.24 1.00 UBIQUITIN-PROTEIN LIGASE 1 1.00 E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; E3A; CHAIN: D; E3A; CHAIN: D; E3A; CHAIN: A, B, C; UBIQUITIN-PROTEIN LIGASE 1 1.00 UBIQUITIN CONJUGATING EXIST CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; E3A; CHAIN: D; E3A	1q	වී	∢	126	233	5.1e-35	0.68	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMAIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
A 212 564 0 131.07 UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	10	Z	A	202	562	0	0.24	1.00		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2: CHAIN: D:	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIOUITIN CONJUGATING ENZYME
115 707 1a.06 0.66 0.05	15	4z	A	212	564	0			131.07	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
A TIS 201 IS-00 10:00 10:00 INECKAL CELL ADHESION	lepf	JC	A	115	207	1e-06	99.0	0.05		NEURAL CELL ADHESION	CELL, ADHESION NCAM: NCAM.

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
NO:	110	O N	I AA	AA		score	score	D score	-	
									MOLECULE; CHAIN: A, B, C, D;	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1575	1ev2	E	113	188	3e-05	-0.30	0.13		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; EIDD ODI A ST CROWTH	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2;
							٠		FIBROBLASI OROW IH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE
1575	Ihng	A	115	212	1.5e-06	0.13	0.04		T LYMPHOCYTE ADHESION GL YCOPROTEIN CD2 (RAT) IHNG 3	DOMESTICS, D'INCE OLD COLD
1575	1tit		113	186	1.2e-05	-0.25	0.00		TITIN, 127; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN
1575	2fcb	A	105	206	7.5e-06	0.13	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1576	1d0s	Ą	484	664	9e-10	80.0	-0.19		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1576	1d0s	A	491	643	7.5e-10	0.14	-0.20		NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A;	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE
1576	Ieut		138	324	1.5e-10	0.05	-0.20		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1576	leut		266	476	6e-10	0.03	-0.19		SIALIDASE; CHAIN: NULL;	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE
1578	1bp3	В	102	212	6e-11	0.02	-0.14		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B:	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1578	1bp3	В	31	224	6e-11			53.09	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR,

PDB annotation	HORMONE/GROWTH FACTOR	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN		HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4- HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE- RECEPTOR COMPLEX	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,
Coumpound	CHAIN: B;	TITIN; CHAIN: NULL;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES	PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;
SEQFOL D score						56.61	57.30	
PMF score		80.0-	-0.09	0.04	-0.14			0.34
Verify score		-0.00	0.08	0.09	0.23			0.30
Psi Blast		9e-10	3e-08	6e-10	3e-10	7.5e-06	1.2e-09	1.2e-09
END		218	211	199	211	315	224	199
STAR T AA		119	124	41	124	35	34	37
CHAI N ID			A		Ф	A		
PDB ID		1bpv	1c8p	1cfb	lf6f	1fnh	1mfn	1mfn
SEQ ID NO:		1578	1578	1578	1578	1578	1578	1578

Coumpound PDB annotation	GLYCOPROTEIN	HAIN: A, B; PIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	CTIN ) TF 3	N; CHAIN: A; PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING		AMINE N- TRANSFERASE  NSFERASE; ACETYLTRANSFERASE	ARCESCENS TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCN5-RFI ATFD N.	ACETYLTRANSFERASE, 3 COA-BINDING	N- TRANSFERASE N-ACETYL TRANSFERASE TRANSFERASE		NSFERASE; COENZYME A COMPLEX, C, D; ACETYLTRANSFERASE
		TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONE (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 11	FIBRONECTIN; CHAIN: A;		ARYLALKYLAMINE N- ACETYLTRANSFERASE; CHAIN: A, B;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;		SEROTONIN N- ACETYLTRANSFERASE; CHAIN: A;	HPA2 HISTONE ACETYLTRANSFERASE;	CHAIN: A, B, C, D;
SEQFOL D score		55.27									
PMF score			0.59	0.10		0.80	0.10		98.0	0.04	
Verify score			-0.03	0.11		0.42	-0.56		0.50	-0.15	
Psi Blast		4.5e-07	1.5e-09	9e <b>-</b> 10		8.5e-14	1.7e-10		5.1e-13	5.1e-12	
END		211	199	213		627	622		627	624	
STAR T AA	-	35	124	124		511	523		511	487	
CHAI N ID		Ą		¥		В	A		Ą	А	
PDB ID		1qr4	1tif	2fnb		1b6b	1504		1cjw	1qsm	
SEQ ID NO:		1578	1578	1578		1579	1579		1579	1579	

PDB annotation		TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AAC; AMINOGLYCOSIDE 6'-N-	ACETYLTRANSFERASE, ANTIRIOTIC 2 RESISTANCE	ACETYL COENZYME A	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE,	EUBACTERIAL 2	AMINOGLYCOSIDE RESISTANCE,	GCN3-RELATED N-ACETYLTRANSFERASE, 3 COA-	BINDING	TRANSFERASE N-ACETYL	TRANSFERASE	SIGNALING PROTEIN P300/CBP	ASSOCIATED FACTOR, COENZYME	A, ACELYLIKANSFEKASE, 2	COACTIVATOR, SIGNALING	The Angelers 4 of the Officers	COENZYME A COMPLEX	ACETYLTRANSFERASE	TRANSFERASE PROTEIN-ACETYL	COENZYME A COMPLEX,	ACETYLTRANSFERASE	TRANSFERASE HISTONE	ACETYLTRANSFERASE, GCN5-	A COUTTY TO A STREET A COL A	ACELIFIKANSFERASE, Z COA BINDING PROTEIN
Coumpound		ARYLALKYLAMINE N- ACETYLTRANSFERASE; CHAIN: A, B;	AMINOGLYCOSIDE N6'- ACETYLTRANSFERASE TYPE	I; CHAIN: A;		SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N-	CHAIN: A, B;	-			SEROTONIN N-	ACETYLTRANSFERASE; CHAIN: A;	P300/CBP ASSOCIATING	FACTOR; CHAIN: B, A;			TWO THE TOWN	ACETVI TRANSFERASE.	CHAIN: A, B, C, D;	HPA2 HISTONE	ACETYLTRANSFERASE;	CHAIN: A, B, C, D;	TGCN5 HISTONE ACETYL	TRANSFERASE; CHAIN: A;		
SEQFOL	D score																									
PMF	score	0.83	0.16			0.04					0.63		0.10				170	t 0:0		0.00			0.48			
Verify	score	0.43	-0.18			-0.18					0.59		0.13				0.17	1.0		80.0			-0.21			
Psi Blast		3.4e-19	1.7e-11			5.1e-12					1.5e-18		Ie-17				2 do 11	2.10-11		1.5e-14			8.5e-16			
END	AA	732	749			727					732		751				770	ì		738			749			
STAR	L WA	616	626			627					610		637				615	3		642			637			
CHAI		В	Ą			A					Ą		В				\ -	<b>:</b>		Ą			Ą			
PDB	<b>1</b>	156 <b>b</b>	1587			1bo4					1cjw		1cm0				loem	mak.		1qsm			ldst			
SEQ	NO:	1580	1580			1580					1580		1580				1580	2		1580			1580			

РDВ annotation	IAIN: A, TRANSCRIPTIONAL REGULATION, HISTONE ACETYLATION, N-2 ACETYLTRANSFERASE, GCN5 RELATED N-ACETYLTRANSFERASE FAMILY, 3 GENE REGULATION	A, B; CALIDOREDUCTASE TRYPANOTHIONE REDUCTASE, FAD DEPENDENT DISULPHIDE 2 OXIDOREDUCTASE	GHAIN: OXIDOREDUCTASE FLAVIN- DEPENDENT AMINE OXIDASE, OXIDOREDUCTASE	<u></u>	NAM DI; SPLICING, SPLICEOSOME, SM, SLEAR CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	NEW BINDING PROTEIN D3 CORE SNRNP SMALL PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC
Coumpound	TRANSCRIPTIONAL ACTIVATOR GCN5; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR
F SEQFOL  e D score							
PMF	0.39	0.21	0.09	0.16	0.63	0.93	0.33
Verify score	-0.37	0.06	0.02	0.01	0.48	0.50	0.50
Psi Blast	5.1e-14	1.2e-06	0.00014	1.5e-07	1.4e-13	3.4e-11	1.7e-11
END	749	116	104	123	126	122	126
STAR T AA	637	65	70	29	44	40	41
CHAI N ID	¥	A	A	Ą	¥	В	Ą
PDB ID	lygh	laog	1537	3lad	1634	1534	1436
SEQ ID NO:	1580	1582	1582	1582	1587	1587	1587

PDB annotation		PROTEIN	RNA BINDING PROTEIN D3 CORF	SURVING PROTEIN: B CORE SURVING	PROTEIN SNRNP SPLICING SM	COPE SUDAD DOMAIN SYSTEMIC	CORE SINGLE DOMALIN, STREMIC TIDIIS 2 ERVITEMATOSIIS SUR	PROTEIN		RNA BINDING PROTEIN D3 CORE	SNRNP PROTEIN; B CORE SNRNP	PROTEIN SNRNP, SPLICING, SM,	CORE SNRNP DOMAIN, SYSTEMIC	LUPUS 2 ERYTHEMATOSUS, SLE,	PROTEIN			OXIDOREDUCTASE PDZ DOMAIN,	NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN,	NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE	PROTEIN	ケ	F; CYTOKINE,		CHEMOATTRACTANT FACTOR, PDZ			KINASE HCASK, GLGF REPEAT,
PDB		RNA BINDING PROTEIN	RNA BINDING I	SNRNP PROTET	PROTEIN SNRN	COPE SYMPHE	TIPLIS 2 ERVT	RNA BINDING PROTEIN		RNA BINDING I	SNRNP PROTEI	PROTEIN SNRN	CORE SNRNP D	LUPUS 2 ERYTH	RNA BINDING PROTEIN			OXIDOREDUCI	NNOS, NITRIC	OXIDOREDUCI	NNOS, NITRIC	PEPTIDE RECO	RECOGNITION, PROTEIN	LOCALIZATION	CYTOKINE LCF; CYTOKINE,	LYMPHOCYTE	CHEMOATTRA	DOMAIN		KINASE HCASK
Coumpound		ASSOCIATED CHAIN: B, D, F, H, J, L;	SMALL NIICLEAR	RIBONITCI EOPROTEIN SM D3:	CHAIN A C E G I K SMAII.	MICHEAD	RIBONI ICI EOPROTEIN	ASSOCIATED CHAIN: B D F H	J. L;	SMALL NUCLEAR	RIBONUCLEOPROTEIN SM D3;	CHAIN: A, C, E, G, I, K; SMALL	NUCLEAR	RIBONUCLEOPROTEIN	ASSOCIATED CHAIN: B, D, F, H,	J, L.;		NEURONAL NITRIC OXIDE	SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	NEURONAL NITRIC OXIDE	SYNTHASE; CHAIN: A;	PSD-95: CHAIN: A: CRIPT:	CHAIN; B;	,	INTERLEUKIN 16; CHAIN:	NULL;				HCASK/LIN-2 PROTEIN;
SEQFOL	D score																													
PMF	score		66 0	1						69.0								96.0		0.82		1.00			0.76					0.93
Verify	score		0.25	}						0.26								0.69		0.72	_	0.56			0.35		•			0.83
Psi Blast			5.1e-24	1						8.5e-25								3e-14		3.4e-13		1.5e-18			1.5e-16					7.5e-15
END	AA		134							134							ç	08		110		98			96					87
STAR	T AA		43	!						39								7.7		3		5			6				-	ر ا
CHAI	OI N		В	I						D								V		Ą		A							,	¥.
PDB	OI		1d3h							q£p1								bsar		1b8q		1be9			1116				11.	IKWa
SEQ	NO:		1587							1587								1288		1588		1588			1588				1000	1388

PDB annotation	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING	PROTEIN BINDING GATE-16; UBIQUITIN FOLD	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
Coumpound	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN; A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	GOLGI-ASSOCIATED ATPASE ENHANCER OF 16 KD; CHAIN: A, B;	APOLIPOPROTEIN A-1; CHAIN: A, B, C, D;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score							54.19	61.70
PMF	1.00	0.95	1.00	66.0	1.00	0.89		
Verify score	0.78	0.89	0.66	0.79	0.91	0.36		
Psi Blast	le-17	1.2e-14	3.4e-19	1.4e-15	1.7e-16	8.5e-34	4.5e-06	1.5e-07
END AA	06	96	81	83	98	187	244	248
STAR T AA	က	12	E	1	3	91	53	28
CHAI N ID		A	A	А	А	A	Y .	A
PDB ID	1pdr	1qau	1qav	1qlc	3pdz	1eo6	laví	lcun
SEQ D NO:	1588	1588	1588	1588	1588	1590	1591	1591

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSPORT PROTEIN VAMP 2; MEMBRANE FUSION PROTEIN COMPLEX, TRANSPORT PROTEIN	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR) COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN
Coumpound	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	SSO1 PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SYNAPTOBREVIN 2; CHAIN: A, E, I; SYNTAXIN 1A; CHAIN: B, F, J; SNAP-25B; CHAIN: C, G, K; SNAP-25B; CHAIN: D, H, L;	DHPI; CHAIN: NULL;	DHP1; CHAIN: NULL;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P; ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;
SEQFOL D score				57.26	55.15			
PMF score	0.45	0.95	0.04			0.16	0.17	0.06
Verify score	-0.00	0.16	0.23			0.49	0.17	0.21
Psi Blast	3.4e-22	1.5e-38	3.4e-13	4.5e-12	9e-24	5.1e-05	3.4e-05	1c-10 4.5e-12
END	233	233	213	251	245	73	75	324
STAR T AA	17	19	22	28	174	30	36	306
CHAI N ID	В	В	A	A	В			1 1
PDB ID	1dn1	1dn1	1fio	lquu	lsfc	4hb1	4hb1	laut
SEQ D	1591	1591	1591	1591	1651	1591	1591	1592

PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR)	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EXTRACELLULAR, MODULAR BEATERI SIBEACE 3 ANTICEN	FROIEIN, SURFACE 2 ANTIQEIN, MALARIA VACCINE COMPONENT	ROTEIN	SURFACE PROTEIN MEROZOITE	SURFACE ANTIGEN 1, MAJOR	BLOOD-STAGE EGF-LIKE DOMAIN,	EAIRACELLULAK, MUDULAK	PROTEIN, SURFACE Z ANTIGEN,	ACCINE COMPONENT,	BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)		BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,	2 RECEPTOR ENZYME, INHIBITOR,	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)	
<u>a</u>	COMPLEX (BLOOD COAGULATION/IN	SURFACE PI SURFACE A	BLOOD-STA	EXTRACELI	MALARIA V	SURFACE PROTEIN	SURFACE PI	SURFACE A	BLOOD-STA	EAIKACELI	PKOLEIN, SO	SURFACE PROTEIN	BLOOD COA	PROTEASE,	2 RECEPTOF	GLA, EGF, 3	PROTEASE/(		BLOOD COA	PROTEASE,	2 RECEPTOF	GLA, EGF, 3	PROTEASE/(		BLOOD COA	PROTEASE,	2 RECEPTOR	GLA, EGF, 3	PROTEASE/(	
Coumpound		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;			-		MEROZOITE SURFACE	PROTEIN 1; CHAIN: A;					BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;	CHAIN: T, U; D-PHE-PHE-ARG-	CHLOROMETHYLKETONE	(DFFRCMK) WITH CHAIN: C:
SEQFOL D score																														
PMF score		0.04					0.04			,			0.09	þ					-0.19						0.16					
Verify score		0.18					90.0						0.44						0.17						0.02					
Psi Blast		1.5e-09					1.5e-14						1.4e-09						3.4e-11						3e-15					
END		326					374						186						249						385					
STAR T AA		246					280						109						139						253					
CHAI N ID		∀					A						7						J						Г					
PDB ID		1cej					1cej						Idan						1dan						1dan					_
SEQ ID NO:		1592					1592						1592						1592						1592					

PDBCHAISTARENDPsi BlastVerifyPMFSEQFOLCoumpoundIDN IDT AAAAscorescoreD score	END Psi Blast Verify PMF SEQFOL  AA score score D score	Psi Blast Verify PMF SEQFOL score Score D score	Blast Verify PMF SEQFOL score score D score	PMF SEQFOL score D score	SEQFOL D score		Coumpound		PDB annotation
Idva         L         109         186         1.4e-09         0.24         -0.03         DES-GLA FACTOR VIIA           (HEAVY CHAIN); CHAIN: H, I;         DES-GLA FACTOR VIIA (LIGHT         DES-GLA FACTOR VIIA (LIGHT           CHAIN: CHAIN: CHAIN: CHAIN: LM; (DPN)-         CHAIN: CHAIN: LM; (DPN)-	186 1.4e-09 0.24 -0.03	1.4e-09 0.24 -0.03	0.24 -0.03	-0.03		DES-GLA FACTOR V. (HEAVY CHAIN); CH. DES-GLA FACTOR VI CHAIN); CHAIN: I, M	DES-GLA FACTOR V. (HEAVY CHAIN); CH DES-GLA FACTOR VI CHAIN); CHAIN: LM	IIA AIN: H, I; IIA (LIGHT ; (DPN)-	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
						PEPTIDE E-76; CHAIN:	PHE-AKG; CHAIN: 0 PEPTIDE E-76; CHA	S, D; IN: X, Y;	
1dva L 139 249 3.4e-11 0.13 -0.18 DES-GLA FACTOR VIIA	249 3.4e-11 0.13 -0.18	3.4e-11 0.13 -0.18	0.13 -0.18	-0.18		DES-GLA FACTOR	DES-GLA FACTOR	VIIA	HYDROLASE/HYDROLASE NITIBITOD DEOTEIN DEDITIDE
DES-GLA FACTOR VIIA (LIGHT	DES-GLA FACTOR V	DES-GLA FACTOR V	DES-GLA FACTOR V	DES-GLA FACTOR V	DES-GLA FACTOR V	DES-GLA FACTOR V	DES-GLA FACTOR V	IIA (LIGHT	COMPLEX
CHAIN); CHAIN: L, M; (DPN)-	CHAIN); CHAIN: L, M	CHAIN); CHAIN: L, M PHE-ARG: CHAIN: C	CHAIN); CHAIN: L, M PHE-ARG: CHAIN: C	CHAIN); CHAIN: T. N	CHAIN); CHAIN: L, N PHE-ARG: CHAIN: C	CHAIN); CHAIN: L, N	CHAIN); CHAIN: L, N PHF-ARG: CHAIN: C	f; (DPN)- r.	
PEPTIDE E-76; CHAIN: X, Y;	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	PEPTIDE E-76; CHAIN	έχ, Υ <u>;</u>	
1 dx5 1 295 383 1.2e-14 -0.18 0.01 THROMBIN LIGHT CHAIN;	383 1.2e-14 -0.18 0.01	1.2e-14 -0.18 0.01	-0.18 0.01	0.01		THROMBIN LIGHT (	THROMBIN LIGHT (	HAIN;	SERINE PROTEINASE
CHAIN: A, B, C, D; THROMBIN	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	CHAIN: A, B, C, D;	THROMBIN	COAGULATION FACTOR II;
HEAVY CHAIN; CHAIN: M, N,	HEAVY CHAIN; O. B. THE CHAIN; O. B. THE CHAIN; O.	HEAVY CHAIN; G	HEAVY CHAIN; G	HEAVY CHAIN; C	HEAVY CHAIN; (	HEAVY CHAIN; (	HEAVY CHAIN; (	CHAIN: M, N,	COAGULATION FACTOR II;
CU, F; THKOMBOMOLDULIN; CHANN: 1 TV 1, THROWED	O, F; THKOMBO	O, F; THKOMBO	O, F; LHKOMBO	O, F; LHKOMBO	O, F; THROMBO	O, F; THROMBO	O, F; LHKOMBO	MODULIN;	ANTIGEN: FOR CAR STREET
CHAIN: 1, 1, K, L; ITROMBIN INHIBITOR L-GLV-L-	INHIBITOR L-G	CHAIN: 1, 1, 15, 15, 16, 17	CHAIN: 1, 1, 15, L	CHAIN: 1, 3, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15	CHAIN: 1, 3, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15	CHAIN; I, J, K, L   INHIBITOR L-GI	CHAIN: 1, J, N, L INHIBITOR L-G	U-L-GLY-L-	AN HOEN; EGR-CMK SEKINE PROTEINASE, EGF-LIKE DOMAINS.
ARM; CHAIN: E, F, G, H;	ARM; CHAIN: E	ARM; CHAIN: E	ARM; CHAIN: E	ARM; CHAIN: E	ARM; CHAIN: E	ARM; CHAIN: E	ARM; CHAIN: E	i, F, G, H;	ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOI VTIC COMPLEX
1dx5 I 307 402 8.5e-12 0.03 -0.15 THROMBIN LIGHT CHAIN;	402 8.5e-12 0.03 -0.15	8.5e-12 0.03 -0.15	0.03 -0.15	-0.15		THROMBIN LIC	THROMBIN LIC	SHT CHAIN;	SERINE PROTEINASE
						CHAIN: A, B, C,	CHAIN: A, B, C,	CHAIN: A, B, C, D; THROMBIN	COAGULATION FACTOR II;
HEAVY CHAIN; CHAIN: M, N,	HEAVY CHAIN	HEAVY CHAIN	HEAVY CHAIN	HEAVY CHAIN	HEAVY CHAIN	HEAVY CHAIN	HEAVY CHAIN	; CHAIN: M, N,	COAGULATION FACTOR II;
O, P; THROMBOMODULIN;	O, P; THROMBC	O, P; THROMBC	O, P; THROMBC	O, P; THROMBC	O, P; THROMBC	O, P; THROMBO	O, P; THROMBO	)MODULIN;	FETOMODULIN, TM, CD141
CHAIN: J, J, K, L; THROMBIN	CHAIN: 1, 1, K, 1	CHAIN: J, I, K, I	CHAIN: I, J, K, I	CHAIN: I, I, K, I	CHAIN: I, I, K, I	CHAIN: I, I, K, I	CHAIN: I, I, K, I	J. THROMBIN	ANTIGEN; EGR-CMK SERINE
INHIBITOR L-GLU-L-GLY-L-ADM: CHAM: B B G U:	J-TINITIBITOR T-C	J-d Infilial OK L-G	JUHIBITOR L-C	J-MAIDII OK L-C	D-TINHIBITOR TO	APM: CHAINE	APM: CUAN:	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	ANTICOACIII ANT COMEITE 2
	ם ייוודוול) (מואה	Third, Other	d vitality (vitality)	d. Charles, trivial	Carrier, Carrier, D		avivi, Cinain.	,1,0,11,	ANTIFIBRINOLYTIC COMPLEX
1emn 245 339 1.7e-09 0.01 -0.05 FIBRILLIN; CHAIN; NULL;	339 1.7e-09 0.01 -0.05	1.7e-09 0.01 -0.05	0.01 -0.05	-0.05		FIBRILLIN; CHA	FIBRILLIN: CHA	AIN: NULL;	MATRIX PROTEIN
							•	`	EXTRACELLULAR MATRIX,
									CALCIUM-BINDING,
									GLYCOPROTEIN, 2 KEPEAT,
									SIGNAL, MULTIGENE FAMILY,
									DISEASE MUTATION, 3 EGF-LIKE

PDB annotation	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MOTATION, 5 EGF-LIKE	POMAIN, HOMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING	BLOOD CLOTHING	COMPLEX/SERINE	PROTEASE/COFACTOR/LIGAND),	BLOOD COAGULATION, 2 SERINE	PROTEASE, COMPLEX, CO-FACTOR,
Coumpound		FIBRILLIN; CHAIN: NULL;						FIBRILLIN; CHAIN: NULL;								FIBRILLIN; CHAIN: NULL;								TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;	BLOOD COAGIT ATTON	FACTOR VIIA: CHAIN: 1.:	BLOOD COAGULATION	FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR;
SEQFOL D score		56.86							•										_					55.46						
PMF						_		0.55								0.13										0.03				
Verify score								0.33								0.36					·					0.10				
Psi Blast		1.7e-15				_		1.7e-15								8.5e-14					<del>, , , , , , , , , , , , , , , , , , , </del>			3e-10		1.4e-09				
END		382						380								402								357		186				
STAR T AA		277						302								337								194		109				
CHAI N ID				_																		•		A		T				
PDB ID		1emn						1emn								lemn								lext		1 fak				
SEQ ID NO:		1592						1592								1592								1592		1592				
											71	3							•											

SEQFOL  CHAIN: T; 5L15; CHAIN: 1;  CHAIN: T; 5L15; CHAIN: 1;  CHAIN: T; 5L15; CHAIN: 1;  BLOOD COAGULATION  BLOOD CLOTTING  BLOOD CLOTTING  BLOOD CLOTTING  BLOOD CLOTTING  BLOOD CLOTTING  COMPLEX(SERINE  BLOOD COAGULATION  FACTOR VIIA; CHAIN: 1;  RECEPTOR EXEYORE, 3 INHIBITOR, 6 COMPLEX (SERINE  SOLUBLE TISSUE FACTOR;  CHAIN: T; 5L15; CHAIN: 1;  RECEPTOR EXEYORATION  BLOOD CLOTTING  CHAIN: T; 5L15; CHAIN: 1;  RECEPTOR EXEYORATION  RECEPTOR EXEYORATION  ILAMININ; CHAIN: NULL;  CLAMININ; CHAIN: NULL;  CLYCOPROTEIN GLYCOPROTEIN  LAMININ; CHAIN: NULL;  CLYCOPROTEIN GLYCOPROTEIN  CLYCOPROTEIN  CLYCOPROTEIN GLYCOPROTEIN  CLYCOPROTEIN  C		
Jog of the state o	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
D score		FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
PMF score 0.00 0.00 0.31 -0.12 -0.14 -0.19 -0.12 -0.19 -0.12		-0.07
Verify score 0.08 0.20 0.15 0.19 0.19 0.07 0.07 0.58		0.44
Psi Blast 3.4e-11 3.4e-12 3.4e-13 3.4e-17 7.5e-19 3.4e-12 1e-11 3.4e-09		1.5e-10
AA AA AAA 380 380 381 381 331 382 396 193 403 173		229
246 139 139 112 112 147 230 231 27 295 109		139
N ID A A A A A A A A A A A A A A A A A A		T
1   1   1   1   1   1   1   1   1   1		xjd1
SEQ D NO: 1592 1592 1592 1592 1592 1592 1592 1592		1592

SEQ PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation	
<b>a</b>		TAA	AA		score	score	D score			
									INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA,	
									SERINE PROTEASE, CALCIUM-	
									BINDING, HYDROLASE, 3 GLYCOPROTEIN	
1qfk	,	109	186	1.4e-09	0.55	-0.09		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;	
								(LIGHI CHAIN); CHAIN: L;	BLOOD COAGULATION, SEKINE	
								COAGULATION FACTOR VIIA	PROTEASE	
_								(HEAV I CHAIN), CHAIN: II, TRIPEPTIDYL INHIBITOR:		
								CHAIN: C;		
1qfk	7	143	249	3.4e-10	0.23	-0.17		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;	
								(LIGHT CHAIN); CHAIN: L;	BLOOD COAGULATION, SERINE	
-								COAGULATION FACTOR VIIA	PROTEASE	
								(HEAVY CHAIN); CHAIN: H;		
								TRIPEPTIDYL INHIBITOR;		
$\dashv$								CHAIN: C;		
1592   1qfk	ப	253	338	7.5e-09	0.26	-0.18		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;	
								(LIGHT CHAIN); CHAIN: L;	BLOOD COAGULATION, SERINE	_
								COAGULATION FACTOR VIIA	PROTEASE	
	···							(HEAVY CHAIN); CHAIN: H;		
								TRIPEPTIDYL INHIBITOR;		
+								CHAIN: C;		
1592   1qfk	<u>, , , , , , , , , , , , , , , , , , , </u>	283	385	1.3e-11	0.49	0.71		COAGULATION FACTOR VIIA	SERINE PROTEASE FVIIA; FVIIA;	
								(LIGHT CHAIN); CHAIN: L;	BLOOD COAGULATION, SERINE	
								COAGULATION FACTOR VIIA	PROTEASE	_
								(HEAVY CHAIN); CHAIN: H;		_
								TRIPEPTIDYL INHIBITOR;		
								CHAIN: C;		
1tpg		128	180	3e-10	0.91	-0.05		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION	
			,					F1-G; 1TPG 7 CHAIN: NULL;		
	,	,						ITPG 8		
1592   1xka	J_	109	681	3.4e-09	0.23	-0.12		BLOOD COAGULATION	BLOOD COAGULATION FACTOR	
								FACTOR XA; CHAIN: L, C;	STUART FACTOR; BLOOD	

PDB annotation	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR	STUANT FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR	STUART FACTOR; BLOOD	DOCTEINASE EDITEDMAL 2	GROWTH FACTOR LIKE DOMAIN										CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
Coumpound		BLOOD COAGULATION	FACTOR AA, CHAIN. L, C,		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;			BLOOD COAGULATION	FACTOR XA; CHAIN: L, C;			LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	(ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	(ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ	(ISOLECTIN 2) 9WGA 3	DNAJ; CHAIN: NULL;
SEQFOL D score								53.26					1000	60.84							81.78
PMF score		£0.0 <del>-</del>			0.46							-0.12				-0.19		-0.05			
Verify score		0.04			0.43							0.22				0.04		-0.00			
Psi Blast		7.5e-09			1.2e-11			1.2e-11				3.4e-14	,	1.3e-16		1.4e-15		3.4e-13			3.4e-28
END AA		328			382	·		395				264	9	340		342		221			11
STAR T AA		255			283			305				114	2.5	701		183		92			-
CHAI N ID		L			$\Gamma$			L				A	*	∢		Ą		A			
PDB ID		lxka			1xka			1xka				9wga		ywga		9wga		9wga			1bq0
SEQ ID NO:		1592			1592			1592				1592	1500	7601		1592		1592			1593

		·	Γ												Ι	_				1	
PDB annotation	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE				COMPLEX (DNA-BINDING	PROTEIN/DNA)						GENE REGULATION/DNA LEF-1	HMG; LEF1, HMG, TCR-A,	TRANSCRIPTION FACTOR, DNA	BINDING, DNA 2 BENDING,	COMPLEX (HMG DOMAIN/DNA), GENE REGIII ATION/DNA	GENE REGULATION/DNA LEF-1	HMG; LEF1, HMG, TCR-A,
Coumpound	DNAJ; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	HUMAN HSP40; CHAIN: NULL;	 DNA-BINDING HIGH MOBILITY GROUP PROTEIN	FKAGMEN I-B (HMGB) (DNA- BINDING 1HME 3 HMG-BOX	DOMAIN B OF RAT HMG1)	HUMAN SRY, 1HRY 6 CHAIN:	A; IHRY 7 DNA; IHRY 9 CHAIN: B; 1HRY 10	DNA-BINDING HIGH	MOBILITY GROUP PROTEIN 1 (HMG1) BOX 2, COMPLEXED	WITH IHSM 3	MERCAPTOETHANOL (NMR,	MINIMIZED AVERAGE STRUCTURE) 1HSM 4	LYMPHOID ENHANCER-	BINDING FACTOR; CHAIN: A;	DNA (5'- CHAIN: B; DNA (5'-	CHAIN: C;		LYMPHOID ENHANCER-	BINDING FACTOR; CHAIN: A;
SEQFOL D score		86.98													125.69						
PMF score	1.00		1.00	1.00	0.43			0.24		0.75										1.00	
Verify score	0.84		76.0	0.97	-0.13			0.01		0.11										0.31	
Psi Blast	3.4e-28	1e-33	3.4e-27	1e-33	1.4e-21			Ie-27		3.4e-22					3e-22					3e-22	
END	89	78	89	77	416	1		416		419	-				429					420	
STAR T AA	3	2	3	3	351			350		351					344					345	
CHAI N ID								A							Ą					A	
PDB ID	1 <b>b</b> q0	1hdj	Ihdj	1hdj	1hme			1hry		1hsm	-				2lef					2lef	
SEQ ID NO:	1593	1593	1593	1593	1594			1594		1594			***		1594					1594	

SEQ ID	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
ÖZ									DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GFNF REGII A TION/DNA
1594	2lef	A	350	420	3.4e-20	0.40	1.00		LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1	,									
1598	1cg7	<b>∀</b>	31	106	8.5e-21	0.10	0.89		NON HISTONE PROTEIN 6 A; CHAIN: A;	DNA BINDING PROTEIN HMG BOX, DNA BENDING, DNA RECOGNITION, CHROMATIN, NMR, DNA 2 BINDING PROTEIN
1598	Ihry	Ą	43	114	le-21	-0.10	0.78		HUMAN SRY; 1HRY 6 CHAIN: A; 1HRY 7 DNA; 1HRY 9 CHAIN: B; 1HRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	Ihry	A	43	115	7.5e-27			83.75	HUMAN SRY; 1HRY 6 CHAIN: A; 1HRY 7 DNA; 1HRY 9 CHAIN: B; 1HRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	1hry	A	44	115	7.5e-27	0.04	0.81		HUMAN SRY; 1HRY 6 CHAIN: A; 1HRY 7 DNA; 1HRY 9 CHAIN: B; 1HRY 10	COMPLEX (DNA-BINDING PROTEIN/DNA)
1598	2lef	∢	43	128	6e-27			57.47	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA
1598	2lef	Ą	44	128	8.5e-17	-0.29	0.74		LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING,

Coumpound PDB annotation	COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'- CHAIN: C; COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA LEF-1 TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	 TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P; GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	FORMIN BINDING PROTEIN; SH3 DOMAIN WW DOMAIN, FBP28, CHAIN: A; SIGNAL TRANSDUCTION	FORMIN BINDING PROTEIN; SH3 DOMAIN WW DOMAIN, FBP28, CHAIN: A: SIGNAL TRANSDUCTION	CHAIN: A: SH3 DOMAIN WW DOMAIN, FBP28, SIGNAI: TRANSDITCTION	CHAIN: A: SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	WWPROTOTYPE; CHAIN: A; SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	WWPROTOTYPE; CHAIN: A; SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	
SEQFOL Co		LYMPHOID ENHANCER-BINDING FACTOR; CHAIDING FACTOR; CHAIDING FACTOR; CHAIN: C;	TRANSDUCIN; CHAIN: P; PHOSDUCIN; CHAIN: P;	FORMIN BIN CHAIN: A;	FORMIN BIN CHAIN: A;	FORMIN BIN	FORMIN BIN CHAIN: A:	WWPROTOT	WWPROTOT	
PMF score		0.71	-0.20	96.0	0.94	06.0	96.0	0.87	0.35	
Verify score		0.27	0.10	09:0	0.72	0.17	60.0	0.03	0.64	
Psi Blast		6e-27	1.5e-09	5.1e-07	1.5e-09	3e-09	8.5e-08	3.4e-09	3,4e-12	
END		116	173	160	161	121	121	159	118	,
STAR T AA		45	0	133	133	87	92	129	85	00
CHAI N ID		∢	<u>ط</u>	A	Ą	A	A	Ą	A	
PDB ID		2lef	2trc	1e0I	1e0I	1e01	1e0I	1e0m	1e0m	,
SEQ ID NO:		1598	1599	1602	1602	1602	1602	1602	1602	1,000

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΑÖ	8	N IS	TAA	AA		score	score	D score		
1602	1f8a	В	132	185	90-99	-0.06	0.01		PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	ISOMERASE PINI; PEPTIDYL- PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
				-					The state of the s	
1603	1e0l	A	06	125	1e-07	-0.19	0.82		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION
1603	1e01	А	96	124	1.5e-09	0.72	0.94		FORMIN BINDING PROTEIN; CHAIN: A;	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION
1603	1e0m	А	96	121	6.8e-05	0.25	66.0		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1603	1e0m	А	96	121	6e-05	0.25	0.99		WWPROTOTYPE; CHAIN: A;	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN
1603	1f8a	В	95	148	90 <del>-</del> 99	-0.06	0.01		PEPTIDYL-PROLYL CIS-TRANS	ISOMERASE PINI; PEPTIDYL-
									ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING
1606	15j4	A	П	387	1.7e-67	0.20	0.78		SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A;	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE
1606	16jn	Ą	26	389	1.7e-58			355.62	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS
1606	1bjn	А	27	389	1.7e-58	0.71	1.00		PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS
1606	Ibt4	A	26		5.1e-60	0.84	1.00		PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, PHOSPHOSFRINF, 2 AT KAT IPHIT IC
1606	1c0n	А	11	389	1.7e-61	0.28	1.00		CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOLD
1606	1cj0	¥.		387	5.1e-67	0.07	0.59		SERINE HYDROXYMETHYLTRANSFER	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE,

PDB         CHAI         STAR         END         Psi Blast         Verify         PMF         SEQFOL           ID         N ID         T AA         AA         AA         score         D score         D score	STAR END Psi Blast Verify PMF TAA AA score score	END Psi Blast Verify PMF AA score score	Psi Blast Verify PMF score	Blast Verify PMF score	PMF	L	SEQFOL D score		Coumpound	PDB annotation
The state of the s					AS	AS	AS	AS	ASE; CHAIN: A, B;	1 CARBON METABOLISM
1dfo A 8 386 1.7e-67 0.11 0.66 SEI HY AS	8 386 1.7c-67 0.11 0.66	386 1.7e-67 0.11 0.66	1.7e-67 0.11 0.66	67 0.11 0.66	0.66		SEI HY AS:	SE HY AS	SERINE HYDROXYMETHYLTRANSFER ASE: CHAIN: A. B. C. D:	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO
										TRANSFERASE, (AAT)-LIKE FOLD
1eji A 1 386 1.7e-66 -0.02 0.42 SE	1 386 1.7e-66 -0.02 0.42	1.7e-66 -0.02 0.42	1.7e-66 -0.02 0.42	66 -0.02 0.42	0.42		ES H	出民	SERINE HYDROXYMETHYLTRANSFER	TRANSFERASE SHMT; SERINE- GLYCINE CONVERSION,
AS	AS	AS	AS	AS	AS	AS	AS	AS	ASE; CHAIN: A, B, C, D;	PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE,
1bj4 A 1 344 3.4e-62 0.15 0.18 SEI	1 344 3,4e-62 0.15 0.18	3.4e-62 0.15 0.18	3.4e-62 0.15 0.18	52 0.15 0.18	0.18		(SE)	S	SERINE	TRANSFERASE TRANSFERASE,
HY	HY	H A A A A A A A A A A A A A A A A A A A	HY ASA	H X	H Y H Y H Y H Y H Y H Y H Y H Y H Y H Y	H.Y.	AS	ΑSΑ	HYDROXYMETHYLTRANSFER ASE: CHAIN: A:	METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE
1bin A 26 343 1.7e-49 PH	26 343 1.7e-49 287 66	343 1.7e-49 282 66	1.7e-49	99 286				밁	PHOSPHOSERINE	AMINOTE ANSFER ASE DSAT.
								₹	AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE, L-SERINE
A,	A,	A,	[A,	(A,	A,	A,	Ą	Ą	A, B;	BIOSYNTHESIS
1bjn A 27 337 1.7e-49 0.58 1.00 PI	27 337 1.7e-49 0.58 1.00	337   1.7e-49   0.58   1.00	1.7e-49 0.58 1.00	1.00	1.00		PI	Ы	PHOSPHOSERINE	AMINOTRANSFERASE PSAT;
<u> </u>	<u> </u>	<u> </u>	<u> </u>	<u> </u>	<u> </u>	<u> </u>	<u> </u>	⋖	AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE, L-SERINE
					A	A	A	<	A, B;	BIOSYNTHESIS
1bt4 A 25 336 5.1e-51 0.59 1.00 P	25 336 5.1e-51 0.59 1.00	336 5.1e-51 0.59 1.00	5.1e-51 0.59 1.00	51 0.59 1.00	1.00		<u>.</u>	Д	PHOSPHOSERINE	TRANSFERASE PSAT;
	4	4	<u> </u>	A	A		A	A	AMINOTRANSFERASE; CHAIN:	AMINOTRANSFERASE,
A	A	A	A	A .	<b>A</b>	Α	Y	⋖	A;	PYRIDOXAL-5'-PHOSPHATE,
								- 1		PHOSPHOSERINE, 2 ALKALIPHILIC
1 A 11 344 8.5e-56 -0.01 0.48	11 344 8.5e-56 -0.01 0.48.	8.5e-56 -0.01 0.48	8.5e-56 -0.01 0.48	56 -0.01 0.48	0.48			$\sim$ 1	CSDB PROTEIN; CHAIN: A;	LYASE ALPHA/BETA FOLD
1cj0   A   1   344   6.8e-62   -0.04   0.43   1	1 344 6.8e-62 -0.04 0.43	6.8e-62 -0.04 0.43	6.8e-62 -0.04 0.43	52   -0.04   0.43	0.43			• .	SERINE	TRANSFERASE SHMT;
	<u>.</u>						_	_	HYDROXYMETHYLTRANSFER	HYDROXYMETHYL TRANSFERASE,
				7	7	7	7	٦	ASE; CHAIN: A, B;	1 CARBON METABOLISM
1dfo A 3 344 5.1e-66 0.07 -0.02	3 344 5.1e-66 0.07 -0.02	344 5.1e-66 0.07 -0.02	5.1e-66 0.07 -0.02	56 0.07 -0.02	-0.02		51	101	SERINE	TRANSFERASE SHMT, SERINE
	<u>-</u>	<u>-</u>	<u>-</u>	<u> </u>	<u> </u>			μ,	HYDROXYMETHYLTRANSFER	METHYLASE; ALPHA PLP
								7	ASE; CHAIN: A, B, C, D;	ASPARTATE, AMINO
										TRANSFERASE, (AAT)-LIKE FOLD
leji A   1   344   5.1e-59   0.07   0.07   5	1 344 5.1e-59 0.07 0.07	5.1e-59 0.07 0.07	5.1e-59 0.07 0.07	59 0.07 0.07	0.07			<i>(</i> (	SERINE	TRANSFERASE SHMT; SERINE-
<u> </u>		T.			H	H		$\Xi$	HYDROXYMETHYLTRANSFER	GLYCINE CONVERSION,

PDB annotation	PYRIDOXAL 5'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER	COMPLEX (TRANSCRIPTION FACTORDNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTORDNA)	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN		LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
Coumpound	ASE; CHAIN: A, B, C, D;	STAT3B; CHAIN: A; 18-MER DESOXYOLJGONUCLEOTIDE; CHAIN: B;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;
SEQFOL D score				70.36			
PMF score		0.04	0.11		0.01	0.22	0.04
Verify score		-0.48	-0.33		-0.23	-0.31	0.05
Psi Blast		0.00051	1.2e-06	7.5e-05	3.4e-11	0.003	6.8e-14
END		20	82	345	603	611	885
STAR T AA			1	96	552	515	828
CHAI N ID		A	А	A		¥	A
PDB ID		1bg1	1fxk	1quu	lchc	1fbv	160x
SEQ ID NO:		1608	1608	1609	1612	1612	1614

PDB annotation	D, E, F, SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER		TA); CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-RINDING PROTEIN					1
Coumpound	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I, CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C CHAIN: A
SEQFOL D score								
PMF score	-0.09	1.00	1.00	0.37	1.00	0.59	0.89	0.00
Verify score	0.21	0.08	0.32	0.33	-0.05	-0.02	0.85	-0.50
Psi Blast	6.8e-15	1.5e-26	4.5e-16	1.5e-36	3e-28	1.2e-08	6.8e-22	1.5e-14
END AA	885	716	864	871	717	721	856	669
STAR T AA	825	588	728	755	588	819	732	909
CHAI N ID	Ą	A	Ą	A	Ą	A	A	A
PDB ID	1b4f	1a25	1a25	1a25	1byn	lbyn	1byn	1djx
SEQ ID NO:	1614	1616	1616	1616	1616	1616	1616	1616

PDB annotation	DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			ENDOCYTOSIS/EXOCYTOSIS C2-
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;
SEQFOL D score									
PMF score		1.00	1.00	66.0	0.17	0.58	1.00	0.59	0.36
Verify score		0.13	-0.11	0.20	0.12	-0.09	0.12	0.39	0.07
Psi Blast		8.5e-59	1.2e-27	4.5e-14	1.7e-39	9e-20	96-30	6.8e-22	3.4e-46
END		875	716	845	872	726	717	856	874
STAR T AA		587	588	728	751	909	288	732	730
CHAI N ID		A	A	A	Ą	-~			A
PDB ID		1dqv	1dsy	Idsy	1dsy	Irlw	Irsy	lrsy	3rpb
SEQ ID NO:		1616	1616	1616	1616	1616	1616	1616	1616

	QI N	TAA	END AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1a25 A	A	230	351	6.8e-27	0.28	0.34		PROTEIN KINASE C (BETA);	CALCIUM-BINDING PROTEIN CALB;
								Chain: A, B,	CALCLOMFF/FROSFINGLIFING BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1a25 A	4	69	197	1.5e-26	90.0	1.00		PROTEIN KINASE C (BETA);	CALCIUM-BINDING PROTEIN CALB;
								O. M. P., D.	CALCUM: MINOSI INCLINIOS BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1a25 A	A	69	208	1.5e-26			59.65	PROTEIN KINASE C (BETA);	CALCIUM-BINDING PROTEIN CALB;
								CHAIN: A, B;	CALCIUM++/PHOSPHOLIPID
									BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN
1byn ≜	A	221	343	6.8e-23	0.26	0.21		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
									SYNAPTOTAGMIN, C2-DOMAIN,
									EXOCYTOSIS,
									NEUROTRANSMITTER 2 RELEASE, FNDOCYTOSIS/FXOCYTOSIS
1byn A	A	69	961	1.7e-27	0.33	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
				_					SYNAPTOTAGMIN, C2-DOMAIN,
		-							EXOCYTOSIS,
									NEUROTRANSMITTER 2 RELEASE,
$\dashv$		,							ENDOCYTOSIS/EXOCYTOSIS
lbyn   A	∢	69	198	3e-28	-0.05	00.1		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS
				•					SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS
				,		,			NEUROTRANSMITTER 2 RELEASE.
									ENDOCYTOSIS/EXOCYTOSIS
lcjy   A	Ą	230	333	1.7e-16	0.13	-0.05		CYTOSOLIC PHOSPHOLIPASE	HYDROLASE CPLA2;
	_	_						A2; CHAIN: A, B;	PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE

nnd PDB annotation		III; CHAIN: ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	C, ALPHA TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	C, ALPHA TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	C, ALPHA TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C			OLIPID 1 (FIRST C2 RSY 3	IOLIPID I (FIRST C2	DCV2
SEQFOL Coumpound	D score	SYNAPTOTAGMIN III; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	7 7
-								69.42		
$\vdash$	score	0.39	0.13	0.70	1.00	0.58	0.07		1.00	_
Verify	score	-0.26	0.24	-0.23	-0.11	-0.09	0.16		0.39	
Psi Blast		3.4e-52	1.2e-28	3.4e-21	1.2e-27	9e-20	6.8e-23	6e-30	1.7e-27	
END	AA -	356	351	203	197	207	343	200	196	
STAR	TAA	71	232	89	69	87	221	62	69	
CHAI	a v	¥_	A	A	A					
PDB	9	1dqv	Idsy	1dsy	ldsy	Irlw	lrsy	Irsy	11rsy	
SEQ	a ö	1617	1617	1617	1617	1617	1617	1617	1617	

SEQ BO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
1617	3rpb	A	236	354	3.4e-27	0.15	0.45		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1617	3rpb	A	71	206	8.5e-20	0.22	0.96		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1618	Ibyn	А	264	366	1.3e-06	0.29	0.17		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1618	1dsy	A	264	356	0.0045	-0.00	0.13		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1618	lrsy		264	366	1.5e-05	0.14	0.16		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1620	1a68		rs.	68	5.1e-26	0.38	1.00		POTASSIUM CHANNEL KV1.1; CHAIN: NULL;	POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY 2 STRUCTURE, APLYSIA KV1.1
1620	1buo	A	ري د	104	6.8e-05	0.65	0.65		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEITEMIA GENE REGIII. ATION	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER	METAL TRANSPORT ION CHANNEL, OXIDOREDUCTASE, BETA SUBUNIT	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X-RAY STRUCTURE, 2 APLYSIA KV1.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 22
Coumpound		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KV1.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score								53.11
PMF score		66.0	66.0	0.82	0.95	1.00	0.01	
Verify score		0.28	0.31	-0.10	0.38	0.55	-0.18	
Psi Blast		3.4e-25	1.5e-26	1.7e-26	1.2e-26	8.5e-29	0.003	0.003
END		68	92	101	101	102	158	212
STAR T AA		(C)	2	rs.	8	2	17	<del>,</del> 4
CHAI N ID		A	ш	Ą	Ą			Ą
PDB ID		Idsx	1exb	Iqdv	1t1d	3kvt	1cun	Icun
SEQ ID NO:		1620	1620	1620	1620	1620	1621	1621

PDB annotation		PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	יין ייטיוסיית ועוידור מת זערוידה ע תחקות
Coumpound	<b>Y</b>	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	THE CITY OF THE COLOR
SEQFOL D score																	58.17				,													
PMF			0.92				0.46					0.75										0.18					0.98					90.0		
Verify			0.35				-0.29	-				90.0										-0.00					0.08					0.44		
Psi Blast			3,4e-33				1.7e-41					3.4e-45					3.4e-45					6.8e-38					1.5e-13					1.5e-11		
END			691				134					165					991					93					134					165		
STAR T AA			109				33					89					89					7					107					135		_
CHAI N ID			° c				ပ					ပ					ر ن	_				ر ن					Ü					ڻ ن		
PDB ID			lmey				lmey					1mey					Imey					1mey					1mey					1mey		_
SEQ ID	NO:		1624				1624					1624					1624					1624					1624					1624		_

	PDB ID	CHAI	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
145		A	110	169	16-14	0.43	0.12		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
145		Ą	69	165	3.4e-17	-0.23	0.25		TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
lubd	-	U	117	169	1.7e-13	0.21	-0.02		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
lubd		o	30	166	5.1e-28			51.82	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)

COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN
YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE: CHAIN: B:	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;
					54.14		52.53
0.42	0.63	0.29	0.10	0.09		0.84	
-0.13	-0.20	0,14	0.03	0.01		0.83	
5.1e-28	3.4e-15	1e-09	6.8e-25	8.5e-21	4.5e-19	4.5e-19	1.5e-14
165	167	165	164	169	186	181	170
. 66	110	105	13	76	56	92	48
ن ن		¥	<b>∀</b>	4	A	A	A
1ubd	2adr	2drp	2gli	2gli	1589	1589	1be9
1624	1624	1624	1624	1624	1627	1627	1627
	1ubd         C         39.         165         5.1e-28         -0.13         0.42         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           INITIATOR ELEMENT DNA;         CHAIN: A, B;         CHAIN: A, B;	1ubd         C         39.         165         5.1e-28         -0.13         0.42         YY1; CHAIN: C, ADENO-ASSOCIATED VIRUS P5           Initial I	1ubd         C         39.         165         5.1e-28         -0.13         0.42         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           2adr         110         167         3.4e-15         -0.20         0.63         ADRI; CHAIN: NULL;           2drp         A         105         165         1e-09         0.14         0.29         COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3           DNA 2DRP 4         DNA 2DRP 4	1ubd         C         39.         165         5.19-28         -0.13         0.42         YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           2adr         110         167         3.40-15         -0.20         0.63         ADRI; CHAIN: NULL;           2drp         A         105         165         10-09         0.14         0.29         COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4           2gli         A         113         164         6.80-25         0.03         0.10         ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	1ubd         C         39.         165         5.1e-28         -0.13         0.42         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           2adr         110         167         3.4e-15         -0.20         0.63         ADR1; CHAIN: NULL;           2drp         A         105         165         1e-09         0.14         0.29         COMPLEX(TRANSCRPTION REGULATION A) TRAMITRACK PROTEIN (TWO TINGER PEPTIDE) COMPLEXED WITH 2DR9 3 DINA 2DR9 4           2gli         A         13         164         6.8e-25         0.03         0.10         ZINC-FINGER PROTEIN GLI; CHAIN: A; DINA; CHAIN: C, D; CHAIN: C, CHAIN: C,	1ubd   C   39   165   5.16-28   -0.13   0.42   YYI; CHAIN: C; ADENO-ASSOCIATED YRIUS PS	1ubd   C   39   165   5.19-28   -0.13   0.42   YYI; CHAIN: C; ADENO-ASSOCIATED YIRUS P5

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										LOCALIZATION
1627	1be9	A	86	153	1.5e-14	0.12	0.24		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1627	1116		35	161	3e-22			70.34	INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1i16		29	157	3e-22	0.39	0.76		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1627	1kwa	₹.	29	149	3e-19	0.55	86.0		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1627	1qau	Ą	29	176	1.2e-20	0.47	0.37		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1627	1qav ^	¥	67	149	66-20	1.02	1.00		ALPHA-I SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA- FINGER, HETERODIMER
1627	1qlc	A		149	3e-22	0.75	1.00		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	1q1c	A	85	143	1.5e-15	0.05	0.17		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1627	3pdz	А	56	143	1.7e-17	0.30	0.65		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS,

1.00  TYROSINE PHOSPHATASE  (PTP-BAS, TYPE 1); CHAIN: A;  APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;  DHP1; CHAIN: NULL;  A, B; RNA (5- RQP-GP-UP-UP-RP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP	PDB CHAI STAR END ID NID TAA AA	STAR	ļ	END		Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1.00  TYROSINE PHOSPHATASE  (PTP-BAS, TYPE 1); CHAIN: A;  (G3.32  APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;  SXL-LETHAL PROTEIN; CHAIN: P, Q;  RP*GP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U											SPECIFICITY 2 OF BINDING
63.32 APOLIPOPROTEIN A-I; CHAIN:  0.01 DHP1; CHAIN: NULL;  A, B, C, D;  XXL-LETHAL PROTEIN; CHAIN:  A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	3pdz A 56 149 4.5e-22 0	56 149 4.5e-22	149 4.5e-22	4.5e-22			0.92	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING
63.32 APOLIPOPROTEIN A-I; CHAIN:  A, B, C, D;  SXL-LETHAL PROTEIN; CHAIN:  A, B; RNA (5'- R(P*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U				7							
0.01  0.78  SXL-LETHAL PROTEIN; CHAIN:  A, B; RNA (5¹- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U	1av1 A 53 258 5.1e-07	53 258	258		5.1e-07				63.32	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT- ACTIVATION
8XL-LETHAL PROTEIN; CHAIN:  A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* (A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* (B, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP* (B, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP* (B, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP* (B, B; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP* (C, B; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP* (C, B; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP* (C, B; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP* (C, B; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	4hb1 325 366 0.0043 0.	366 0.0043	366 0.0043	0.0043		0	0.12	0.01		DHP1; CHAIN: NULL;	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE
0.78  A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* L1.00  SXL-LETHAL PROTEIN; CHAIN: P, Q; A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*U											
R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	167f A 51 128 1.7e-16 0.78	51 128 1.7e-16	128 1.7e-16	1.7e-16	9	0.7	8	0.78		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00										R(P*GP*UP*UP*GP*UP*UP*	REGULATION, RNP DOMAIN, RNA
74.65 SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP				7						UP*UP*UP*UP*U). CHAIN: P, Q;	COMPLEX
R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	1b7f A 68 231 1.5e-36	68 231	231		1.5e-36				74.65	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
1.00 SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*UP*UP*UP* POLYDENYLATE BINDING PROTEIN 1; CHAIN: P, Q; E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A										R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*U)- CHAIN: P. O:	REGULATION, RNP DOMAIN, RNA COMPLEX
1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00	1b7f A 70 229 1.5e-36 0.91	70 229 1.5e-36	229 1.5e-36	1.5e-36		0.91		1.00		SXL-LETHAL PROTEIN; CHAIN:	RNA-BINDING PROTEIN/RNA TRA
1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00										A, D, MIA (3 - D, MIA (10 - M)	FRE-WINNA; SPLICING
1.00 POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T; O, P, Q, R, S, T; POLYDENYLATE BINDING F F G H: RNA (5'- F F G H: RNA (5'-										K(r*Gr*Ur*Ur*Gr*Ur*Ur* UP*UP*UP*UP*U)- CHAIN: P, Q;	KEGULATION, KNP DOMAIN, KNA COMPLEX
PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	1cvj A 58 148 3.4e-20 0.96	58 148 3.4e-20	148 3.4e-20	3.4e-20		0.96		1.00		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
E, F, G, H; KNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, F F G H: RNA (4'-										PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
K(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, F F G H. RNA (4).										E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
APPAPAATA)-3 J; CHAIN: M, N, O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN J; CHAIN: A, B, C, D, F F G H: RNA (4).										R(*AP*AP*AP*AP*AP*AP* AP*AP*A>A	REGULATION/RNA
POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, F F G H, RNA (4).										AF*AF*AF*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	
I: A, B, C, D,	1cvj A 70 237 1.7e-34	70 237	237		1.7e-34	Ł			81.71	POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
									-	PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,

PDB annotation	PEGIII ATTOMBNA	NEOUZATIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PROCESTIONINA PR	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA		GENE REGIT ATTON/BNA POLY(A)	PRIDING DOCTEN 1 DADS 1. DDM	PROTEIN-RNA COMPLEX GENE	DEGILI ATTONIBNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)
Coumpound	D/* AD* AD* AD* AD* AD* AD*	AP*AP*AP*3); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	POI YDENYI ATE BINDING	DOCTEM 1. CHARL A D C D	F F G H. RNA (5.	D /* A D * A D * A D * A D * A D * A D *	A D*AD*AD*A).3% CHAIN: M N	O. P. O. R. S. T.	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING
SEQFOL	D score					<u> </u>		75.65												52.68									•			
PMF	a loos		1.00											1.00												1.00						1.00
Verify	score		68.0											0.71												0.41						0.36
Psi Blast			1.7e-34					16-30	000					1e-30						1e-33						5.1e-27						1e-33
END	¥		233					218	21					202						212						202				<del></del> -		206
STAR	I AA		71					70	2				_	71						70						71						73
CHAI	O N		Ą					a	3					В						ഥ						Щ						F
PDB	ПТ		lcvj					1cvi	G A					1cvj						Icvj						1cvj						1cvj
SEQ	NO.		1629					1629	707					1629						1629						1629						1629

PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	HNRNP AI; CHAIN: NULL;	HNRNP A1; CHAIN: NULL;
SEQFOL D score		53.52	-	,		
PMF score			1.00	0.99	1.00	1.00
Verify score	1		0.35	0.51	0.69	1.05
Psi Blast		1.4e-31	8.56-2.7	1.4e-31	3.4e-25	3.4e-56
END		209	202	209	144	229
STAR T AA		70	71	72	52	92
CHAI N ID		Ξ	H	н		
PDB ID		Icvj	levj	levj	Iha1	Ihai
SEQ ID		1629	1629	1629	1629	1629

Iba    66   230   3.4e-56   167.63   HNRNP AI; CHAIN: NULL;     Ihd    A   71   144   3.4e-27   1.26   1.00   RIBONUCLEOPROTEIN DO;     Iba    A   71   145   1.5e-27   1.29   1.00   RIBONUCLEOPROTEIN DO;     Iosm   A   235   329   1.5e-11   1.27   -0.19   PHOSPHOPORIN (PHOS) IPHO3     Iqm9   A   22   145   6e-17   0.55   0.23   BINDING PROTEIN SEX-     Isa    61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN SEX-     Isa    62   156   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-     Isa    64   64   64   64   64   64   64	0	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
Ihal   66   230   3.4e-56   167.65   HNRNP AI, CHAIN: NULL;		<b>a</b>	e N	TAA	AA		score	score	D score		
Ihal   66   230   3.46-56   167.63   HNRNP AI; CHAIN: NULL;											RIBONUCLEOPROTEIN
1hd   A   71   144   3.46-27   1.26   1.00   HETEROGENEOUS NUCLEAR RIBONUCLE OPROTEIN DO; CHAIN: A; CHAI	0	1ha1		99	230	3.4e-56			167.63	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN
Ihdi											RIBONUCLEOPROTEIN A1.
Ihdi											NUCLEAR PROTEIN, HNRNP, RBD,
Ihdi											RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
Ihd1   A   71   145   1.5e-27   1.29   1.00   HETEROGENBOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN; A; CHAI	6	1hd1	A	71	144	3.4e-27	1.26	1.00		HETEROGENEOUS NUCLEAR	RNA BINDING PROTEIN RNA-
1hd  A 71   145   1.56-27   1.29   1.00   HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A; CHAIN: CHA										RIBONUCLEOPROTEIN D0; CHAIN: A;	BINDING DOMAIN
10sm   A   235   329   1.5e-11   1.27   -0.19   OMPK36; CHAIN: A, B, C;     1pho   241   324   1.5e-11   1.08   -0.19   PHOSPHOPORIN (PHOE) 1PHO 3     1qm9   A   22   145   6e-17   0.55   0.23   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;     1sx    61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN SEX-BINDING DOMAIN 1SXL 3     18x    61   150   6e-25   0.65   0.60   RBD-2), RESIDUES 199 - 294     15x    62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-BINDING PR	1629	1hd1	A	7.1	145	1.5e-27	1.29	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
10sm   A   235   329   1.5e-11   1.27   -0.19   OMPK36; CHAIN: A, B, C;     1pho   241   324   1.5e-11   1.08   -0.19   PHOSPHOPORIN (PHOE) 1PhO 3     1qm9   A   22   145   6e-17   0.55   0.23   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;     1sxl   61   150   6e-25   0.66   0.60   RINA-BINDING PROTEIN SEX-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3   (RBD-2); RESIDUES 199-294     1sxl   62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-SEX-SEX-SEX-SEX-SEX-SEX-SEX-SEX-SEX-	Ī			-						CHAIN: A;	
1pho   241   324   1.5e-11   1.08   -0.19   PHOSPHOPORIN (PHOE) 1PHO 3     1qm9   A   22   145   6e-17   0.55   0.23   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;     1sxl   61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN SEX-TERMINUS, OR SECOND RNA-BINDING PROTEIN ISXL 3     18xl   62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-TERMINAL MET) 1SXL 5     1sxl   62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-TERMINAL MET) SEX-TERMINUS PROTEIN SEX-TERMINAL MET) SEX-TERMINUS PROTEIN SEX-TERMINUS PR	1629	losm	A	235	329	1.5e-11	1.27	-0.19		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN
1pho   241   324   1.5e-11   1.08   -0.19   PHOSPHOPORIN (PHOE) IPHO 3     1qm9   A   22   145   6e-17   0.55   0.23   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;   15x    61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN (C-TETHAL PROTEIN (C-TETHAL PROTEIN (C-TETHAL PROTEIN (C-TETHAL PROTEIN (C-TETHAL PROTEIN (C-TETHAL PROTEIN SXL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 195 - 294   PLUS N-TERMINAL MET) 18XL 3   (RBD-2), RESIDUES 1											PROTEIN, NON-SPECIFIC PORIN,
A 22 145 6e-17 0.55 0.23 POLYPYRIMDINE TRACT-BINDING PROTEIN CHAIN: A; BINDING PROTEIN; CHAIN: A; BINDING PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5 5 RNA-BINDING PROTEIN SEX-BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 5 5 RNA-BINDING PROTEIN SEX-BINDING P											OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
19m9 A 22 145 6e-17 0.55 0.23   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A; BINDING PROTEIN; CHAIN: A; BINDING PROTEIN (C-TETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN 18XL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 18XL 4 (NMR, 17 STRUCTURES) 18XL 5 15xl 15xl 1.76-16 0.71 0.45   RNA-BINDING PROTEIN SEX-BINDING PROTEIN	29	1pho		241	324	1.5e-11	1.08	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
15x  61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN; CHAIN: A;   ETHAL PROTEIN SEX-   TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5   15x  62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-	65	1qm9	A	22	145		0.55	0.23		POLYPYRIMIDINE TRACT-	RIBONUCLEOPROTEIN PTB. PTB.
15x  61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN SEX-   LETHAL PROTEIN (C-   TERMINUS, OR SECOND RNA-   BINDING DOMAIN 1SXL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL   4 (NMR, 17 STRUCTURES) 1SXL   5   15x  62   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-										BINDING PROTEIN; CHAIN: A;	C198, HETEROGENEOUS NUCLEAR
15x    61   150   6e-25   0.66   0.60   RNA-BINDING PROTEIN SEX-   LETHAL PROTEIN (C-   TERMINUS, OR SECOND RNA-   BINDING DOMAIN 15XL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 15XL   4 (NMR, 17 STRUCTURES) 15XL   5   150   1.7e-16   0.71   0.45   RNA-BINDING PROTEIN SEX-											POLYPYKIMIDINE IKACI BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSI ATION
	67	lsxl		61	150	6e-25	99.0	09.0		RNA-BINDING PROTEIN SEX-	
1sxl 62 150 1.7e-16 0.71 0.45										LETHAL PROTEIN (C.	
1sxl 62 150 1.7e-16 0.71 0.45										BINIDING DOMAIN 18XI 3	
1sxl 62 150 1.7e-16 0.71 0.45										(RBD-2), RESIDUES 199 - 294	
1sxl 62 150 1.7e-16 0.71 0.45										PLUS N-TERMINAL MET) 1SXL	
1sxl 62 150 1.7e-16 0.71 0.45				,						4 (NMR, 17 STRUCTURES) 1SXL 5	
	63	1sxl		62	150	1.7e-16	0.71	0.45		RNA-BINDING PROTEIN SEX-	

PDB annotation		INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3
Coumpound	LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score		·			165.44	70.15
PMF		-0.20	1.00	1.00		
Verify score		1.23	1.05	1.18		
Psi Blast		9e-13	1e-28	5.1e-57	5.1e-57	5.1e-36
END		328	144	233	239	229
STAR T AA		237	22	64	64	69
CHAI N ID			Ą	Ą	∢	A
PDB ID		2omf	2up1	2up1	2up1	3sxl
SEQ ID NO:		1629	1629	1629	1629	1629

Coumpound PDB annotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	SEX-LETHAL; CHAIN: A, B, C; BINDING DOMAIN, RBD, RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	HAIN: A,B,C; COAGULATION/CRYSTAL STRUCTURE/HEPARIN-B FACTOR IIA; COAGULATION/CRYSTAL STRUCTURE/HEPARIN-BINDING STRUCTURE/HEPARIN-BINDING STR/ 2 HIRUDIN/THROMBIN INHIBITOR	A GEI SOLIN: CONTRACTII E PROTEIN MIXED		A GELSOLIN; CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN-BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN		MATING-TYPE PROTEIN A-1; COMPLEX (TWO DNA-BINDING CHAIN: A; MATING-TYPE PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING DNA; CHAIN: C; PROTEINS/DNA), COMPLEX, 2 DNA-BINA
Cour		SEX-LETHAL;	THROMBIN; CHAIN: A,B,C; THROMBIN; CHAIN: D,E,F; HAEMADIN; CHAIN: 1,1,K;	HORSE PLASMA GELSOLIN:	CHAIN: A, B	HORSE PLASMA GELSOLIN; CHAIN: A, B		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B DNA; CHAIN: C;
SEQFOL D score						876.96		
PMF		1.00	0.98	1.00				56.0
Verify score		0.88	0.77	0.81				45.0
Psi Blast		5.1e-36	900.0	0	,	0		9e-06
END AA		229	84	715		715	0	130
STAR T AA		70	47	8		۶.		06
CHAI N ID		A	H	A		Ą		∢
PDB ID		3sxl	le0f	1d0n		1d0n	7	lakn 
SEQ ID NO:		1629	1635	1637	ma V··	1637		1641

							T	
PDB annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION		DNA-BINDING PROTEIN	
Coumpound	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP 3	OCT-3; 1OCP 5 CHAIN: NULL; 10CP 6	DNA BINDING PROTEIN OCT-I POU HOMEODOMAIN DNA- BINDING PROTEIN MUTANT WITH 1POG 3 ARG GLY SER HIS MET INSERTED AT THE N- TERMINUS AND ASP ILE 1POG 4 INSERTED AT THE C- TERMINUS (INS(RGSHM- R6),INS(I66-DI) 1POG 5 (NMR,
SEQFOL D score								
PMF score	0.55	0.33	0.49	86.0	86.0	69:0	0.62	0.78
Verify score	0.22	-0.02	0.17	68:0	0.71	0.33	99'0	0.46
Psi Blast	7.5e-06	1.5e-05	1.5e-06	1.2e-05	9e-06	90 <del>-</del> 99	1.3e-06	3e-06
END	134	136	134	134	134	134	134	134
STAR T AA	92	92	55	92	92	83	92	83
CHAI N ID	A	В		Ą	В			
PDB ID	lau7	1672	1bw5	1fjl	1£]	Ihdp	locp	lpog
SEQ ID NO:	1641	1641	1641	1641	1641	1641	1641	1641

PDB annotation																																	
Coumpound		13 STRUCTURES) 1POG 6	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE	AND INHIBITED 1LPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO	CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIPASE	AND INHIBITED 1LPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO	CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIPASE	AND INHIBITED 1LPB 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO	CONFORMATIONS) 1LPB 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	PROCOLIPASE B 1PCN 3 (NMR,	MINIMIZED AVERAGE	STRUCTURE) 1PCN 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	PROCOLIPASE B 1PCN 3 (NMR,	MINIMIZED AVERAGE	STRUCTURE) IPCN 4	LIPASE PROTEIN COFACTOR
SEQFOL D score																50.95																	56.60
PMF score			0.81						0.88														1.00					1.00					
Verify score			-0.36						-0.35										-				-0.36	_				-0.36					
Psi Blast			8e-19						3e-20							3e-20							3.2e-20					6e-22					6e-22
END			64					ļ	9							99							69					69					69
STAR T AA			29						29							. 8							29					29					2
CHAI N ID			A						₹							A	•									-							
PDB ID			11pb						11pb							11pb							1pcn					lpcn					1pcn
SEQ ID	NO:		1653					0.00	1653							1653							1653					1653					1653

PDB annotation			COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHOTRANSFERASE, PHOSPHORYLATION	SIGNALING PROTEIN/TRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMMETRIC CELL DIVISION	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO- ONCOGENE, PHOSPHOTRANSFERASE	
Coumpound		PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GI.U-(N,N- DIPENTYL AMINE); CHAIN: C, D:	PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE V. SRC TYROSINE KINASE
SEQFOL	D score							
PMF	score		0.03	0.06	0.11	0.95	0.01	0.04
Verify	score		-0.10	-0.06	-0.37	0.08	-0.32	-0.17
Psi Blast			3.2e-28	3.2e-29	3.2e-27	3e-17	3.2e-44	9.6e-29
END			66	102	66	247	165	66
STAR	T AA	,	-		_	120	-	
CHAI	O N		A			¥		۷.
PDB	a -		1a09	I bkl	1bij	1ddm	1fmk	1sha
SEQ	NO.		1654	1654	1654	1654	1654	1654

PDB annotation		COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3
Coumpound	TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SHC; CHAIN: A; TRKA RECEPTOR PHOSPHOPEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;
SEQFOL D score				51.48	
PMF		0.10	0.93		0.98
Verify score		0.17	0.21		0.34
Psi Blast		0.00075	96-24	96-24	0.00032
END AA		247	247	248	260
STAR T AA		110	108	108	110
CHAI N ID		¥	A	∢	Ą
PDB ID		1shc	2nmb	2nmb	2nmb
SEQ ID NO:		1654	1654	1654	1654

PDB CHAI STAR END Psi Blast D N ID T AA AA	STAR END Psi BI TAA AA	END Psi Bl	Psi Blas		Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation REGITI ATTOM
									NEGOLATION
2ifi 29 149 1.6e-44	149		1.6e-44				141.21	EIF1; CHAIN: NULL;	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR
2ifi 42 149 1,6e-44 0.42	149 1.6e-44	1.6e-44		0.42		1.00		EIF1; CHAIN: NULL;	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR
1d2n A 186 257 1.6e-11 -0.15	257 1.6e-11	1.6e-11		-0.15		0.36		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1g41 A 140 260 1.3e-17 -0.14	260 1.3e-17	1.3e-17		-0.14		0.13		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1fmk 334 426 4.8e-22 -0.13	426 4.8e-22	4.8e-22		-0.13		0.45		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1gbq A 335 386 9.6e-15 0.09	386 9.6e-15	9.6e-15		0.09		0.17		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1gbr A 335 392 1.6e-15 0.09	392 1.6e-15	1.6e-15		0.09		0.59		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	

PDB annotation		SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 IGRI 14	COMPLEX (KINASE/PEPTIDE)	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN	TRANSPORT PROTEIN SERINE-RICH RNA POL YMERASE I SUPPRESSOR PROTEIN; ARM REPEAT	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-
Coumpound	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN 2 (GRB2) IGFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) IGFC 4	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	P56=CK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	ABL TYROSINE KINASE; CHAIN: NULL;	KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN: C, D, E, F;	BETA-CATENIN; CHAIN: NULL;
SEQFOL D score								
PMF	0.83	0.35	0.28	60.0	0.96	-0.06	0.41	0.10
Verify score	0.40	-0.64	0.30	0.20	0.43	0.03	60.0	0.02
Psi Blast	6.4e-15	6.4e-16	1.4e-18	1.6e-21	1.6e-16	4.8e-16	3e-05	7.5e-10
END	389	389	425	426	389	426	416	530
STAR T AA	333	304	334	333	330	327	36	107
CHAI N ID		A	Ą	A	А		Ą	
PDB ID	1gfc	1gri	11ck	1qcf	Isem	2abi	lee4	2bct
SEQ ID NO:	1663	1663	1663	1663	1663	1663	1669	1669

PDB annotation	CATENIN, STRUCTURAL PROTEIN	R; COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	R; COMPLEX (INHIBITOR/NUCLEASE) V; COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	N: Q, COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	N: Q, COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN		oʻ	
Coumpound		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: B, D; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: B, D; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: B, D; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: B, D; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;
SEQFOL D score								
PMF score		0.27	1.00	0.40	0.74	0.37	0.34	0.82
Verify score		0.16	0.54	0.10	0.36	0.41	-0.03	0.28
Psi Blast		6.4e-12	1.5e-37	1.5e-19	9.6e-07	1e-23	1.5e-22	9e-20
END		362	314	301	131	171	230	301
STAR T AA		27	29	126	27	30	53	126
CHAI N ID		A	A	A	A	A	A	ပ
PDB ID		la4y	la4y	1a9n	la9n	Ia9n	1a9n	1a9n
SEQ ID NO:		1671	1671	1671	1671	1671	1671	1671

							1		T .	Τ,	-
PDR annotation		COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONICI, EOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP.RIBONICI.EOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIPONICI FOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCL EOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL A DHESTON	
Commonnd		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	
SKOFOL	D score										
PMF	score	0.60	0.00	0.95	0.84	0.01	0.57	0.94	0.93	1.00	
Verify	score	0.50	0.13	0.24	0.40	0.44	0.16	0.70	0.18	0.31	
Psi Blast		4.5e-24	0.00064	9e-18	9.6e-07	9e-24	6e-23	1.6e-23	1.6e-21	6e-14	
END	AA	299	342	334	131	174	240	290	381	106	
STAR	TAA	171	216	220	27	30	53	138	173	29	
CHAI	NID	ပ	၁	ပ	၁	၁	၁	Ą	A	A	
PDB	er e	1a9n	1a9n	1a9n	1a9n	la9n	la9n	1406	1d0b	1406	
SEO	, e s	1671	1671	1671	1671	1671	1671	1671	1671	1671	

PDB annotation	REPEAT, CALCIUM BINDING, CELL ADHESION	: A; CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	: A; CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION		TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- CANSFE FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- CANSFE FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT	TRANSFERASE CRYSTAL ANSFE STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,
Coumpound		INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT;
SEQFOL D score							
PMF score		1.00	1.00	1.00	0.36	1.00	0.89
Verify score		0.74	0.61	0.49	0.18	99'0	0.68
Psi Blast		1.3e-27	8e-28	4.8e-14	3.2e-06	4.8e-10	4.8e-12
END AA		196	242	250	107	130	154
STAR T AA		43	70	145		27	48
CHAI N ID		А	А	A	¥	¥	A
PDB ID		1d0b	140b	1dce	1 dce	1dce	1dce
SEQ ID NO:		1671	1291	1671	1671	1671	1671

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ö	<u>e</u>	<u> </u>	TAA	AA	_	score	score	D score		
									RASE BETA SUBUNIT; CHAIN: B, D;	SUBUNIT, BETA SUBUNIT
1671	1ds9	A	154	289	1.6e-13	-0.03	0.11		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1671	1ds9	Ą	165	299	1.4e-21	-0.14	69.0		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
						-			A;	RICH REPEAT, BETA-BETA-ALPHA
					,					CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1671	1ds9	A	201	380	6.4e-10	-0.32	0.01		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
									A;	RICH REPEAT, BETA-BETA-ALPHA
										CILINDER, DINEIN, Z CHLAMYDOMONAS, FLAGELLA
1671	1ds9	A	27	148	1.6e-12	0.03	0.64		OUTER ARM DYNEIN: CHAIN:	CONTRACTILE PROTEIN LEUCINE-
									A;	RICH REPEAT, BETA-BETA-ALPHA
										CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1671	1ds9	¥	59	195	3.2e-16	0.09	0.52		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
	_								A;	RICH REPEAT, BETA-BETA-ALPHA
					-					CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1671	1f88	В	403	702	1.5e-14	-0.04	0.05		RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN
										PHOTORECEPTOR, G PROTEIN-
			-							COUPLED RECEPTOR, MEMBRANE
										PROTEIN, 2 RETINAL PROTEIN,
	,		l c			100				VISUAL FIGMENT
1671	101 101	A	27	83	8e-05	0.27	0.72		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP.RBD
										OR RRM) AND LEUCINE-RICH-
										REPEAT 2 (LRR)
1671	1fo1	∀	45	107	1.1e-05	-0.08	0.22		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFXI); RIBONUCLEOPROTEIN (RNP,RBD
										OR RRM) AND LEUCINE-RICH-

SEQFOL  D score  NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B; GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B; CHAIN: A, B; CHAIN: NULL; CHAIN: B, D; CHAIN: CHAIN: B, D; CHAIN: CHAIN: B, D; CHAIN: CHA	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRK, LEUCINE-RICH REPEAT, SCF, UBIOUITIN. 2 E3.
SEQFOL D score	¬ 22 ⊠
	CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45;
9000 0.90 0.25 0.25 0.21 0.34 0.34	9C.U
Verify score 0.32 0.32 0.41 0.41 0.19	-0.0-
Psi Blast 1.1e-05 1.5e-16 6e-50 3e-31 3e-31	1.36-08
AA 107 107 154 314 424 424 129 129	771
29 29 29 29 29 29 29 29 29 29 29 29 29 2	76
CHAI N ID B B	¢
PDB 1D 2bnh 2bnh 2bnh 2bnh 1f51 1f51 1f51	1611
SEQ ID NO: 1671 1671 1671 1671 1671 1671 1673	7,01

PDB CHAI STAR ID NID TAA		ST? T A	A A	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation	
										INHIBITOR	
lehd A 104 192	104		192		1.2e-17	0.87	0.01		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	
1ehd A 10 100	10		100		1.2e-19	1.43	-0.14		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	
172 A 84 172	84		172		3e-18	1.28	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	
1eis A 10 116	10		116		1.5e-18	1.17	-0.18		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	
leis A 124 192	124	_	192		1.3e-14	0.05	-0.12 r		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	
1eis A 3 86	ς.		98		7.5e-18	1.32	0.15		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	
1eis A 64 142	64		142		1.5e-19	1.70	-0.14		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	
leis A 77 172	77		172		3e-18	1.37	-0.17		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	
len2 A 104 192	104		192		1e-18	0.98	-0.14		AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	
1en2 A 10 106	10		100		3e-17	1.34	-0.12		AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	
len2 A 3 86	3		98	$\Box$	1.1e-16	1.29	0.15		AGGLUTININ ISOLECTIN	SUGAR BINDING PROTEIN UDA;	

PDB annotation	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-
Coumpound	JAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	OMPK36; CHAIN: A, B, C;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score			59.75				!	84.67	50.00		
PMF score		0.01		-0.19	-0.20	0.05	-0.15			-0.20	-0.20
Verify score		1.54		0.74	0.85	1.09	1.39			1.57	0.33
Psi Blast		3e-18	3e-15	3e-15	6e-25	3e-25	6e-24	3e-25	le-11	4.5e-14	4.5e-19
END AA		172	199	197	200	199	159	160	200	138	201
STAR T AA		74	47	49	10	35	3	4	46	2	42
CHAI N ID		Ą	A	A	A				<b>V</b>	А	ı
PDB ID		Ien2	lext	lext	ligr	1klo	Iklo	Ikio	Incf	losm	1pfx
SEQ IB NO:		1676	1676	1676	1676	1676	1676	1676	1676	1676	1676

SEQ PDB 1D 1D NO:	B CHAI	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									BINDING, HYDROLASE, 3 GLYCOPROTEIN
1qub	b A	m	200	1,4e-30	0.83	-0.20		HUMAN BETA2- GL YCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPI FMENT CONTROL PROTEIN
		·							2 N-GLYCOSYLATION, MULTI- DOMAIN, MEMBRANE ADHESION
1676 1skz	N	13	168	6e-15	0.92	-0.15		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTA SIN CPOSTA I
									STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1676 1skz	2	74	175	1.1e-15	1.27	0.29		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN. CRYSTAL.
									STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1676 1skz	2	93	198	6e-21	0.53	-0.12		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL
					-				STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR. THROMBOSIS
1676 1skz	2	83	202	6e-21			66.09	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR;
	,		*********						ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE
	-	-	102	# T	7	0		THE PROPERTY OF THE PROPERTY O	INHIBITOR, THROMBOSIS
1676 Ivmo	01 ————	<del>-</del>	10/	1.5e-14	1.30	-0.20		MEMBRANE PROTEIN VITELLINE MEMBRANE OLITER I AVER PROTEIN I	

PDB annotation				OXIDOREDUCTASE ALPHA-BETA- ALPHA MOTIF, FLAVIN	CONTAINING PROTEIN, OXIDASE	FLAVOENZYME FLAVOENZYME, NAD BIOSYNTHESIS, FAD, OXIDOREDIICTASE	OALL COLLEGE COLLEGE	OXIDOREDUCTASE ADK, NADPH:	ADRENODOXIN	OXIDOREDUCTASE;	FLAVOENZYME, MAD ANALYSIS,	ELECTRON TRANSFERASE	OXIDOREDUCTASE TETRAHEME	FLAVOCYTOCHROME C	FUMARATE REDUCTASE, 2	OXIDOREDUCTASE	OXIDOREDUCTASE IRON-SULFUR	FLAVOPROTEIN, ELECTRON	TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE IRON-SULFUR	FLAVOPROTEIN, ELECTRON	TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE LIPOAMIDE	DEHYDROGENASE, L PROTEIN, E3,	DLDH, DIHYDROLIPOAMIDE	DEHYDROGENASE, MULTIENZYME	COMPLEX 2 PROTEIN, PYRUVATE	DEHYDROGENASE COMPLEX,	GLYCINE 3 DECARBOXYLASE	COMPLEX, FLAVOPROTEIN
Coumpound	1VMO 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3		D-AMINO ACID OXIDASE; CHAIN: A;		L-ASPARTATE OXIDASE; CHAIN: A;		ADKENODOXIN KEDUCIASE;	CHAIN: A;				FLAVOCYTOCHROME C	FUMARATE REDUCTASE;	CHAIN: A;		TRIMETHYLAMINE	DEHYDROGENASE; CHAIN: A,	_B;	TRIMETHYLAMINE	DEHYDROGENASE; CHAIN: A,	B;	DIHYDROLIPOAMIDE	DEHYDROGENASE; CHAIN: A,	B, C, D;					
SEQFOL D score		101.83					1000	62.05																						
PMF score				0.19		0.13					•		0.36				0.12			0.70			0.00							
Verify score				-0.46		-0.05							-0.03				-0.09			-0.08			-0.41							
Psi Blast		4.5e-23		0.00048		0.00014	1	3.2e-37					3.2e-09				1.6e-12			9e <b>-</b> 13			0.003							
END AA		681		39		46	I i	/27					318				182			359			118							
STAR T A A		8		11		7	0,	O.T					142				2			5			2							
CHAI N ID		Ą		A		A		¥					Ą				A			A			Ą							
PDB ID		9wga	_	1c0p		1chu							1d4d				1djn			Idju			1dxl							
SEQ ID NO:		1676		1680		1680	000,	1080					1680				1680			1680			1680							

SRQ         PDB         GTAM         STAM         FAB         PARIE         FARIE BLANK         Verify Power         Power         Commpound         PDB annotation           1080         1.0         1.0         A.1         4.62         3.2e-94         -0.07         0.29         DHYDROGIENASE; CHAIR, A.         DEHYDROGIENASE; CHAIR, B.         COMPLEX			r · · ·					
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation	OXIDOREDUCTASE LIPOAMIDE DEHYDROGENASE, L. PROTEIN, E3, DLDH, DIHYDROLIPOAMIDE DEHYDROGENASE, MULTIENZYME COMPLEX 2 PROTEIN, PYRUVATE DEHYDROGENASE COMPLEX, GLYCINE 3 DECARBOXYLASE COMPLEX, FLAVOPROTEIN	COMPLEX (OXIDOREDUCTASE/TRANSFERASE ) E3BD; REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE	OXIDOREDUCTASE FLAVOENZYME, OXIDASE, ENANTIOMERIC SPECIFICITY, 0-2 AMINOBENZOATE, ACTIVE SITE FUNNEL, HELICAL DOMAIN, FAD- 3 BINDING DOMAIN			OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE, FLAVOPROTEIN, FAD. NADP	OXIDOREDUCTASE REDOX-ACTIVE CENTER, OXIDOREDUCTASE,
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF	Counipound	DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B, C, D;	DIHYDROLIPOAMIDE DEHYDROGENASE; CHAIN: A, B; DIHYDROLIPOAMIDE ACETYLTRANSFERASE; CHAIN: C;	L-AMINO ACID OXIDASE; CHAIN: A, B, C, D, E, F, G, H;	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCSD) 1FCD 3	ELECTRON TRANSPORT(FLAVOCYTOCHR OME) FLAVOCYTOCHROME C SULFIDE DEHYDROGENASE (FCSD) 1FCD 3	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;
PDB   CHAI   STAR   END   Psi Blast   Verify	SEQFOL D score					83.15		
100	PMF score	0.39	69.0	0.04	0.22		0.51	-0.01
PDB   CHAI   STAR   END   Psi	Verify score	-0.07	-0.04	-0.50	0.10		0.11	0.00
PDB   CHAI   STAR   ID   NID   TAA   S   A   S   A   A   A   A   A   A	Psi Blast	3.2e-94	1.6e-95	1.6e-07	1.6e-19	1.6e-19	7.5e-05	1.6e-74
PDB   CHAI   ID   N I	END AA	462	462	49	407	394	118	459
PDB  IDXI  1 1dxi  1 1dxi  1 1fcd  1 1fcd  1 1fcc  1 1fcc  1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	STAR T AA	<b>&amp;</b>	14	9	10	6	2	8
	CHAI N ID	<b>A</b>	Ą	A	<b>4</b>	∢	A	A
SEQ ID	PDB ID	1dxl	1ebd	1f8s	1fcd	1fcd	1fec	Ifec
	SEQ ID NO:	1680	1680	1680	1680	1680	1680	1680

PDB annotation	FLAVOPROTEIN, FAD, NADP FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE,	OXIDOREDUCTASE OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE	OXIDOREDUCTASE COMPLEX II; COMPLEX II; COMPLEX II; COMPLEX II; FUMARATE REDUCTASE, COMPLEX II, SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE	
I I	FLAVOPROTEIN, FA FLAVIN FLAVIN, PH HYDROXYLASE, MONOOXYGENASE, OXMODEDITION OF	OXIDOREDO OXIDOREDO COMPLEX II, REDUCTASE SUCCINATE RESPIRATIO	OXIDOREDU COMPLEX II, COMPLEX II, REDUCTASE SUCCINATE RESPIRATIO	
Coumpound	PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D, P; CHAIN: D, P;	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT; CHAIN: A, M; FUMARATE REDUCTASE IRON-SULFUR PROTEIN; CHAIN: B, N; FUMARATE REDUCTASE 15 KD HYDROPHOBIC PROTEIN; CHAIN: C, O; FUMARATE REDUCTASE 13 KD HYDROPHOBIC PROTEIN; CHAIN: D. P:	OXIDOREDÚCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH IL.PF 3 FLAVIN-ADENINE- DINIICI FOTTIDE (FA IV. 11 P. 12
SEQFOL D score				
PMF score	0.05	0.37	0.05	0.15
Verify score	-0.79	-0.74	-0.56	-0.25
Psi Blast	0.00032	3.2e-06	0.00032	3.2e-95
END AA	43	43	391	462
STAR T AA	12	12	310	∞
CHAI N ID	4	∢	<b>A</b>	∢
PDB ID	1foh	1fum	1fum	lipf
SEQ ID NO:	1680	1680	1680	1680

PDB annotation	1.8.1.4) NB- 1LVL 4	02(A)) 'X; VITH	AIN: OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 PLAVOPROTEIN, FAD, P64K			.1.8.1.4)	TRANSCRIPTION INHIBITOR BETA- IN: A, PROPELLER	IN: A, PROPELLER	GT-ALPHA/GI-ALPHA COMPLEX (GTP- CHIMERA; CHAIN: A; GT- BINDING/TRANSDUCER) BETA1,
Coumpound	DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) COMPLEX WITH 1LVL 3 NICOTINAMIDE-ADENINB- DINUCLEOTIDE (NAD+) 1LVL 4	OXIDOREDUCTASE (H2O2(A)) NADH PEROXIDASE (NPX) (E.C.1.11.1.1) MUTANT WITH CYS 42 INHP 3 REPLACED BY ALA (C42A) INHP 4	SURFACE PROTEIN; CHAIN: NULL;	L-ALANINE DEHYDROGENASE; CHAIN: A;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-
SEQFOL D score		76.88							
PMF			0.22	0.11	0.06	0.35	10.0	0.99	-0.14
Verify score			-0.06	0.02	-0.43	-0.06	0.25	0.56	0.43
Psi Blast		1.6e-57	6.4e-88	0.0048	6.4e-05	3.2e-91	1.6e-61	3.2e-72	1.4e-55
END		418	463	177	49	462	479	624	476
STAR T AA		12	9	145	4	8	173	304	155
CHAI N ID				A	А	A	A	А	В
PDB ID		lnhp	lojt	1pjc	1408	31ad	lerj	lerj	1got
SEQ ID	NO:	1680	1680	1680	1680	1680	1681	1681	1681

	<del></del>					
PDB annotation	GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	
Coumpound	CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	OMPK36; CHAIN: A, B, C;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3
SEQFOL D score		74.60				
PMF score			0.71	-0.20	-0.18	-0.20
Verify score			0.76	0.86	1,11	06.0
Psi Blast		1.46-55	3.2e-74	4.5e-10	1.5e-12	1.2e-11
END AA		524	621	79	18	80
STAR T AA		179	302	W	∞	4
CHAI N ID		В	æ	4	A	
PDB ID		1got	lgot	Iosm	losm	1pho
SEQ ID NO:		1681.	1681	1685	1685	1685

PDB annotation	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN		CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOLDING. ATPASE	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOLDING, ATPASE	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN	TRANSFERASE PYRUVATE KINASE, GLYCOLYTIC ENZYME, HOMOTETRAMER, 2 TRANSFERASE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
Coumpound	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	ALPHA SPECTRIN; CHAIN: A, B, C;	HYDROLASE CYTIDINE DEAMINASE (CDA) (E.C.3.5.4.5) COMPLEXED WITH ICTT 3 3,4- DIHYDROZEBULARINE (DHZ) ICTT 4	THERMOSOME; CHAIN: A, B;	THERMOSOME; CHAIN: A, B;	GROEL; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N;	PYRUVATE KINASE; CHAIN: A, B, C, D, E, F, H, G;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
SEQFOL D score									
PMF score	-0.19	0.04	0.22	1.00	1.00	0.72	0.23		-0.19
Verify score	1.14	-0.05	-0.02	-0.12	-0.29	-0.14	-0.18	İ	0.06
Psi Blast	1.3e-10	0.00015	9.6e-27	8e-55	6.4e-51	1.6e-68	0.0008		1.4e-09
END AA	08	210	124	186	186	186	106		114
STAR T AA	80	86	14	15	20	12	ъ		33
CHAI N ID		A		A	В	A	A		A
PDB ID	2omf	lcun	1ett	1a6d	1a6d	1 der	1pkl		Jaih
SEQ ID NO:	1685	1688	1690	1692	1692	1692	1692		1696
			760						

PDB annotation	PROTEIN	COMPLEX (ZINC FINGER/DNA)	_		FROIEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	_		REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN
Coumpound	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SILE; CHAIN; B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;	
SEQFOL D score											:																						
PMF		-0.14				-0.18					-0.17					-0.12					-0.19								-0.14				
Verify score		0.07			to	0.07					0.10					0.16					0.08								0.04				
Psi Blast		6.4e-27			0,00	3.2e-19					8e-35					1.1e-09					1.4e-13								3.2e-28				
END		168				114					142					114					138								168				
STAR T AA		06			,	31					19					87					69								63				
CHAI N ID		A				<u>ر</u>					ت ت					Ü					Ą								ပ				
PDB ID		lalh			-	Imey					lmey					Imey	_				1#3					***************************************			lubd				
SEQ ID NO:		9691			1000	16%					1696					9691					1696								1696				

PDB annotation	(TRANSCRIPTION REGULATION/DNA)	IEIN GLII; COMPLEX (DNA-BINDING  HAIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI;  GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	Ö	 , O	(NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONTICLEOPROTEIN	$\vdash$		(NUCLEAR PROTEIN/RNA), RNA,	1	IAIN: A; CELL ADHESION LEUCINE RICH REPEAT. CALCIUM BINDING. CELL	ADHESION	TRANSFERASE CRYSTAL				JNII; GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-							
Coumpound Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q,	R; U2 A'; CHAIN: A, C; U2 B";	CHAIN: B, D;	the state of the s	INTERNALIN B; CHAIN: A;		RAB	GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT:		CHAIN: A, C; RAB	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN:	CHAIN: A, C; RAB GERANYLGERANY RASE BETA SUBUN B, D;	CHAIN: A, C; RAB GERANYLGERANY RASE BETA SUBUN B, D; RAB	CHAIN: A, C; RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN: B, D; RAB GERANYLGERANYLTRANSFE	CHAIN: A, C; RAB GERANYLGERANYLTR, RASE BETA SUBUNIT; C B, D; RAB GERANYLGERANYLTR, RAB GERANYLGERANYLTR,	CHAIN: A, C; RAB GERANYLGERANY RASE BETA SUBUN B, D; RAB GERANYLGERANY RAB GERANYLGERANY RASE ALPHA SUBU CHAIN: A, C; RAB
SEQFOL D score								_							_								
PMF		-0.11	0.94	0.00		96.0				9. 		1.00	_					·		1.00	1:00	00.1	1.00
Verify score		0.03	0.03	-0.34		0.29				0.51		89.0								0.22	0.22	0.22	0.22
Psi Blast		4.8e-17	6.4e-13	6e-11		6.4e-13.			00	1.4e-28		3.2e-15								3.2e-17			
END		144	115	140		115			25.	140		114								137	137	137	137
STAR T AA		7	8	43		18			0,	8	İ	14								39	39	39	39
CHAI N ID		A	⋖	₹		ပ				∢		¥				_	_			A	. <b>4</b>	. <b>4</b>	. <b>4</b>
PDB ID		2gli	1a9n	1a9n		1a9n			101	Idub		1dce							,	1dce	1dce	Idce	1dce
SEQ ID NO:		1696	1698	1698		1698			1,00	1098		1698								1698	1698	1698	1698

D Psi Blast Verify PMF SEQFOL Score score D score
8e-23 -0.55 0.24
133 3e-09 -0.36 0.21 GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;
139 9.6e-10 0.06 0.49 RIBONUCLEASE INHIBITOR; CHAIN: NULL;
0.84 1.00
143 1.2e-56 0.78 1.00 TARGET OF MYB1; CHAIN: A, B;
268 1.4e-22 0.09 -0.06 SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP
481 6.4e-30 0.96 1.00 SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP
307 3.2e-31 0.05 -0.15 POLYDENYLATE BINDING

	<u>_</u>	J.	~ 4	, T	C F	<b>€</b>
PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C; D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*
SEQFOL D score						
PMF score		0.93	1.00	1.00	1.00	1.00
Verify		0.69	1.28	66.0	0.98	1.29
Psi Blast		4.8e-19	4.5e-28	4.8e-25	4.56-24	4.8e-24
END		411	485	487	468	473
STAR T AA		310	331	331	331	331
CHAI N ID		Y	Ą	∢	В	В
PDB ID		1cvj	1cvj	1cvj	Icvj	Icvj
SEQ ID	NO:	1700	1700	1700	1700	1700

PDB annotation		GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM.	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA		GENE REGIT ATTON/BNA DOI V(A)	BINDING PROTEIN 1 PARP 1 RRM	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RIBONUCLEOPROTEIN UIA117;	RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING	DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR RIBONIICI FORBOTEIN 41
Coumpound	O, P, O, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN; A. B. C. D.	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	POI VDENVI ATE RINDING	PROTEIN I CHAIN: A B C D	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;		UI SMALL NUCLEAR	RIBONUCLEOPROTEIN A;	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;			HNRNP A1; CHAIN: NULL;	
SEQFOL D score																													
PMF score		0.64				0.07	5					1.00						0.71	0.83	0.00		0.58			0.37			-0.17	
Verify score		0.46				0.27	1					0.72						0.30	0.93	0.55		0.71	_		0.82			0.26	
Psi Blast		4.8e-25		-		6.4e-26	2					3e-21						3.2e-22	1.6e-17	3.2e-16		3e-17			1.5e-16			4.8e-31	
END		216				233	}					461						208	409	209		417			412			301	
STAR T AA		128				128	) 					331						126	327	127		323			321			126	
CHAI N ID		ഥ				三	<u> </u>			-		H						V	∢	Ą					₹				
PDB ID		lcvj				1cvi	7					1cvj						1d8z	1d8z	1d9a		15t		,	Itjc			lha]	
SEQ ID		1700				1700						1700			_			1700	1700	1700		1700		0000	00/1			1700	

-	(								T		- (										_	Γ			
PDB annotation	NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN AT, NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA- BINDING DOMAIN									ï				
Coumpound		HNRNP A1; CHAIN; NULL;		·	HNRNP A1; CHAIN: NULL;				HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN DO;	CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO;	CHAIN: A;	RIBONUCLEOPROTEIN	PROTEIN FROM UT SMALL	RIBONI ICI EOPROTEIN (SNRNP	111) 1NRC 3 (N-TERMINAL)	FRAGMENT. RESIDUES 1 - 95)	MUTANT WITH GLN 85 INRC 4	REPLACED BY CYS (Q85C)	INRC 5	RIBONUCLEOPROTEIN	PROTEIN FROM UI SMALL	NUCLEAR	RIBONUCLEOPROTEIN (SNRNP
SEQFOL D score																									
PMF score		-0.19			0.99				0.77			0.98		0.49								0.43			
Verify score		0.17			0.78				0.82			98.0		-0.09								-0.19			
Psi Blast		1.6e-20	-	-	1.4e-34				4.8e-23			1.3e-20		1.6e-12								1.3e-12			
END		405			481				206			399		209								207		_	
STAR T AA		226			325				127			331		127								127			
CHAI N ID	İ					_			A			∢		¥						_		Д			
PDB ID		1ha1			1ha1				1hd1			1hd1		Inrc	a							lmrc			
SEQ ID NO:		1700			1700				1700			1700		1700								1700		_	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ö	<u>a</u>	9	TAA	AA —		score	score	D score		
									UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C)	
1700	1qm9	A	128	217	4.8e-09	0.25	-0.14		POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
1700	[sx]		126	211	1.4e-15	0.06	0.33		RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	
1700	lurn	A	323	406	6e-16	0.71	0.99		U1A SPLICEOSOMAL PROTEIN; IURN 5 CHAIN: A, B, C; IURN 6 RNA 21MER HAIRPIN (5'. (AP*AP*UP*CP*CP*AP*UP* IURN 11 CHAIN: P, Q, R IURN 13	COMPLEX (RIBONUCLEOPROTEIN/RNA)
1700	2mss	A	127	206	3.2e-18	0.59	0.10		MUSASHII; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1700	2sxl		. 126	210	1.3e-20	0.47	0.11		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING
1700	2sxl		328	411	1.1e-17	0.82	0.84		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING
1700	2u1a		322	406	4.5e-16	0.60	96.0		UI SMAIL NUCLEAR RIBONUCLEOPROTEIN A;	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN,

Coumpound PDB annotation	VULL: NUCLEAR PROTEIN	SPLICING FACTOR U2AF 65 KD RNA-BINDING PROTEIN SPLICING, U2 SUBUNIT; CHAIN: A; PROTEIN PROTEIN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; RIBONUCLEOPROTEIN/DNA), RIBONUCLEOPROTEIN/DNA), RIBONUCLEOROUS NUCLEAR 2 RIBONUCLEOROUS NUCLEAR 2 RIBONUCLEOROUS NUCLEAR 2 RIBONUCLEOROUS NUCLEAR 2	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; RIBONUCLEOPROTEIN A1 RIBONUCLEOPROTEIN A1 RIBONUCLEOPROTEIN A1 RIBONUCLEOPROTEIN A1	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B; RIBONUCLEOPROTEIN/DNA), RIBONUCLEOPROTEIN/DNA), RIBONUCLEOPROTEIN/DNA), RIBONUCLEOPROTEIN/DNA), RIBONUCLEOPROTEIN A1	SEX-LETHAL; CHAIN: A, B, C; BINDING DOMAIN, RBD, RNA BROGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	
	CHAIN: NULL	SPLICING SUBUNIT;	HETEROG RIBONUCI CHAIN: A; SINGLE-ST TELOMETI	HETEROG RIBONUCI CHAIN: A; SINGLE-ST TELOMETI	HETEROG RIBONUCI CHAIN: A; SINGLE-ST TELOMETI	SEX-LFTH	TUMOR SUPPRESSOR
SEQFOL D score							67.76
PMF score		0.05	-0.19	-0.14	0.87	1.00	
Verify score		0.53	0.01	0.35	0.49	1.01	
Psi Blast		9.6e-13	1.1e-34	4.8e-22	1,3e-35	3.26-29	4.5e-30
END		206	311	410	484	474	191
STAR T AA		127	126	226	325	329	35
CHAI N ID		Ą	4	A	∢	Ą	
FDB ID		2u2f	2up1	2up1	2up1	3sxl	la5e
SEQ ID	5	1700	1700	1700	1700	1700	1701

																											_
PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN.	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) GABPALPHA;   GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN. ETS DOMAIN.	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABFBEIAI; COMFLEX	(IKANSCKIPIJON	REGULATION/DNA), DNA-BINDING,	ANKYRIN REPEATS.	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETAI; COMPLEX
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PNA: CHAIN: B;	DINA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;
SEQFOL D score																									90.41		
PMF score				1.00						1.00							1.00										
Verify score				0.94						06.0							1.11										
Psi Blast				1.1e-40						3e-39							1.6e-37								3e-45		
END AA				298						165							165								363		
STAR T AA				150						15							17	100							212		
CHAI N ID		·		В	·												Д								 		
PDB ID	 			lawc						Iawc			_				lawc								lawc		
SEQ ID NO:				1701						1701	_						1701								1701		

		BINDING, DOMAIN,	2	NA ALPHA;		BINDING,	DOMAIN,	2	N.	ALPHA;		BINDING,	DOMAIN,	ı	~	Z. :	ALPHA;		BINDING.	DOMAIN,	`	×   5	AI DHA.	(	
PDB annotation		ON ONA), DNA OTEIN, ETS	AIS, N3FACTO	NSCRIPTI( NA) GABP	OMPLEX	NA), DNA-	OTEIN, ETS ATS,	N 3 FACTO	NSCRIPTI	NA) GABP MPI FX	. N.	NA), DNA-	OTEIN, ETS	ATS,	N 3 FACTO	NSCRIPTIC	NA) GABP	JMFLEA	JA NA). DNA-	OTEÍN, ETS	ATS,	N 3 FACTO	INSCRIETA INA) GABD		MPLEX
PDB		(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANK YKIN KEPEAIS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA; GARPRETAI: COMPIEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	KEGULATION/DNA) GABPALPHA;	CABPBEIAI; COMPLEX	REGULATION/DNA), DNA-BINDING.	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	COMMITTY (THE ANISOTRIETION)	REGIII ATTON/DNA) GABBAI PHA:		(TARPHELAI-COMPLEX
Coumpound		DNA; CHAIN: D, E;	:	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA: CHAIN: D. E;				GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	FROIEIN BEIA I; CHAIN: B; DNA: CHAIN: D F:				GA BINIDING BROTEIN AT BITA:	CHAIN: A. GA BINDING		PROTEIN BETA 1: CHAIN: B:
SEQFOL	D score	Ω		0 0					10		<u> </u>	_		•		<b>5</b> 0	<u>ة</u> ت		) 					_	Id.
PMF	score			1.00					1.00				_			1.00				-		00	2	_	
Verify	score			0.64					0.25							1.07				_	-	0.46	2		
Psi Blast				1.2e-41					3.2e-32				-			le-32						66-30	)	_	
END	AA			395					427							405						100	3		
STAR	TAA			212					250							8/2					_	45	?		
CHAI	QI N			B					В						,	<b>a</b>						E C	1		
PDB	<u>e</u>			lawc					lawc							Iawc						1awe	<u> </u>	_	
SEO	NO:			1701					1201						,	10/1						1701		_	

	Z.				۲۳			7	_														_						
PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR
Coumpound		GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B; DNA: CHAIN: D F:				P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;
SEQFOL D score											87.58																		
PMF score		1.00						1.00						1.00			1.00			0.77			1.00			1.00			1.00
Verify		0.72						0.42						0.85			0.81			0.39			0.67			0.44			0.80
Psi Blast		4.8e-37						3e-37			1.4c-38			7.5e-38			1.5e-37			1.4e-38			4.5e-30			1.4e-36		,	1.4e-38
END		199						299			301			168			333			397		- 0	405			201			234
STAR T AA		50						113			145			17			183			215		3	279			46			82
CHAI N ID		В																											
PDB ID		1awc						1bd8			1bd8			1bd8			1bd8		:	1bd8		5	1 pd8			lpd8	-		lbd8
SEQ ID NO:		1701						1701			1701			1701			1701			1701		700	1701			1701		,	1701

									Τ	_												•				_
PDB annotation	ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN CYCL BY THE PROTEIN	FROIEIN, CICLIN-DEFENDENI KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	AIDHADETA COMES CONTROL,	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	しょうしょうていしい ニュース・ファン・ファン・プログラング しょうかい
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: D.	D;		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B:	â		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	, n			CYCLIN-DEPENDENT KINASE 6. CHAIN: A. PIGINKAD: CHAIN:	B:				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	В;			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	Ġ.
SEQFOL D score					80.38																					
PMF score		1.00							1.00					1.00					1.00					1.00		
Verify score		0.72							0.92					0.48					0.43					0.32		
Psi Blast		9e-38			1.5e-39		-		1.5e-39					1.4e-38					3e-39					9e-38		
END AA		271			170				170					338					401					205		
STAR T AA		114		_	12				13					183					215					46		
CHAI N ID		В			В				В					В					<u>я</u>					В		
PDB ID		1blx			1blx				1blx					1blx					1blx					16lx		
SEQ ID NO:		1701			1701				1701					1701					1701					1701		

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1701	1bu9	¥	253	432	3.2e-30	0.24	0.25		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C; TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE GEOWETH PACTOR
1701	1bu9	A	6	177	1.36-35			92.05	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1701	1d9s	A	104	237	3e-37	09:0	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
1701	1d9s	Ą	269	401	1.5e-36	0.80	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN; A;	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT
1701	111/6	A	253	431	1.4e-29	0.43	0.93		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1701	11hb	A	81	236	9e-38			89.22	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1701	likn	D	145	371	1.2e-53	0.19	0.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1701	likn	D	17	173	1.5e-39	0.71	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBNFKB COMPLEX

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΘŠ	<b>a</b>	01 N	TAA	AA		seore	score	D score		
									B-ALPHA; CHAIN: D;	
1701	likn	Q	212	427	1.1e-38	0.05	0.92		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
									CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA: CHAIN: D:	IKB/NFKB COMPLEX
1701	likn	D	215	403	3e-50	0.49	0.99		NF-KAPPA-B P65 SUBUNIT:	TRANSCRIPTION FACTOR P65:
			i 		}		}		CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	1ikn	Ω	45	232	4.8e-43	0.11	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
									CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	likn	Ω	45	240	4.5e-52	0.13	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
							_		CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN; C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	likn	Ω	45	253	4.5e-52			81.35	NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
									CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	likn	Ω	82	276	4.5e-52	0.28	0.99		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
						4			CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
1701	lmyo		247	391	1.5e-30	0.26	0.71		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
										ACETYLATION, NMR, ANK-REPEAT
1701	Infi	ш	113	311	9e-51	0.58	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
								_	Ę.	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1701	Infi	ы	143	401	3e-49	0.10	66.0		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-NAFFA-B P30; CHAIN: B, D;	KEG/AINK KEPEAL) COMPLEX

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ŝ	a .	NID	TAA	AA		score	score	D score		
									I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1701	lnfi	Щ	17	170	4.5e-39	0.94	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
1701	Infi	កា	210	427	1.16-38	0.42	0.70		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRN 2 REPEAT HE! IX
1701	Infi	[1]	42	242	1.5e-51			87.55	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX
1701	lnfi	ਬ	43	238	1.5e-51	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YR IN 2 REPEAT HE! IX
1701	Infi	ъ	44	232	6,4e-43	0.59	00.1		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX
1701	1sw6	А	61	287	4.5e-36	-0.06	0.28		REGULATORY PROTEIN SW16; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1701	1sw6	A	76	320	4.5e-36			70.20	REGULATORY PROTEIN SWI6; CHAIN: A, B;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE

PDB annotation	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN		PROTEIN KINASE CDK2; PROTEIN
Coumpound	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	TRANSFERASE (PHOSPHOTRANSFERASE) \$C-/AMP\$-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	CYCLIN-DEPENDENT PROTEIN
SEQFOL D score	70.78				
PMF score		0.55	0.65	0.86	0.11
Verify score		-0.07	0.08	0.30	0.22
Psi Blast	7.5e-35	4.5e-37	1.6e-70	6.4e-98	1.1e-46
END AA	396	283	303	312	266
STAR T AA	214	81	31	29	29
CHAI N ID	В	В		ш	
PDB ID	lycs	1ycs	1a06	lapm	lad1
SEQ ID NO:	1701	1701	1702	1702	1702

EQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
8 B	Œ	NID	TAA	AA		score	score	D score	•	
									KINASE 2; CHAIN: NULL;	KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1702	163u	A	231	416	0.0003	0,22	1.00		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1702	163u	A	278	560	1.4e-33	0.29	1.00		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1702	lcmk	<u> </u>	29	312	3.2e-99	0.10	0.75		PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	
1702	1ctp	Ħ	29	303	8e-94	0.01	0.86		TRANSFERASE (PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1702	1f3m	ပ	29	264	3.26-49	0.35	0.98		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1702	Ihel		29	266	4.8e-49	0.26	0.60		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1702	Iial	Ą	328	551	6e-05	0.26	0.24		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	PDB annotation
UO:	ID	NID	TAA	AA	•	score	score	D score	4	
										ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1702	1koa		59	304	1.3e-58	0.30	0.75		TWITCHIN; CHAIN: NULL;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1702	1kob	А	55	265	8e-57	0.51	96'0		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1702	1p38		3	334	3.2e-42			81.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1702	1phk		31	264	6.4e-71	0.48	0.99		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING
1702	lvrk	Ą	301	453	1.1e-19	-0.18	0.09		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1702	2bct		438	560	0.0001	-0.31	0.52		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA- CATENIN, STRUCTURAL PROTEIN
1704	liku		308	440	0.0003	-0.04	0.07		RECOVERIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCUIM-BINDING PROTEIN
1705	1bu2	A	157	352	3.2e-26	-0.26	0:30		CYCLIN HOMOLOG; CHAIN: A;	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL

1		TON A-BOX E- EIN-DNA FOLD, YTA-BOX,	4- EDK2, P33 CCN1; N, CDK, 2	IN, CELL TORY- TEIN	OR BETA-	BETA1, UNIT; GAMMA P-
PDB annotation	CYCLIN	TRANSCRIPTION/DNA TRANSCRIPTION INITIATION FACTOR IIB, TFIIBC; TATA-BOX FACTOR, TATA SEQUENCE- BINDING PROTEIN, PROTEIN-DNA COMPLEX, CYCLIN-LIKE FOLD, HELIX-TURN-HELIX, 2 TATA-BOX, TRANSCRIPTION/DNA	COMPLEX (PROTEIN KINASE/CYCLIN) CYCLIN- DEPENDENT KINASE-2, CDK2, P33 PROTEIN KINASE; CCNA, CCN1; COMPLEX (PROTEIN KINASE/CYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE COMPLEX	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY- SUBUNIT, 2 BINDING PROTEIN	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G
Coumpound		GENERAL TRANSCRIPTION FACTOR IB; CHAIN: A, E, I, M, Q; TATA BOX BINDING PROTEIN; CHAIN: B, F, J, N, R; ADMLP TATA-BOX DNA CONTAINING IIB RECOGNITION CHAIN: C, G, K, O, S; ADMLP TATA-BOX DNA CONTAINING IIB RECOGNITION CHAIN: D, H, L, P, T.	CELL DIVISION PROTEIN KINASE 2; CHAIN: A, C; GZ/MITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	CYCLIN A; CHAIN: NULL;	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;
SEQFOL D score						
PMF score		0.17	0.01	0.04	1.00	0.93
Verify score		-0.02	-0.21	-0.11	0.65	0.35
Psi Blast		1.3e-23	4,8e-49	4.8e-48	8e-67	1.4e-59
END		350	345	345	571	529
STAR T AA		183	136	142	277	230
CHAI N ID		<b>Y</b>	ш		A	В
PDB ID		1c9b	1qmz	Ivin	lerj	lgot
SEQ ID NO:		1705	1705	1705	1708	1708

PDB annotation	SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)		COMPLEX (PROTO- ONCOGENE/EARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SHZ DOMAIN, SIGNAL TRANSDUCTION,
Coumpound		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C, D;	TRANSFERASE (PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1AB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SH2 ABL) 1AB2 4 (NMR, 20 STRUCTURES) 1AB2 5	FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYL PEPTIDE; CHAIN: P
SEQFOL D score		104.96				
PMF score			1.00	0.09	0.12	0.06
Verify score			0.55	0.56	0.38	0.47
Psi Blast		1.6e-69	1.6e-69	8e-25	1.6e-22	4.8e-21
END		695	695	380	382	378
STAR T AA		242	280	282	282	282
CHAI N ID		æ	В	A		Ħ
PDB ID		1got	lgot	1a09	1ab2	laot
SEQ ID NO:		1708	1708	1709	1709	1709

A 242 379 5.26-26 0.08 score score score score score score 284 385 1.6e-24 0.29 0.01 0.07 1.6e-22 0.31 0.07 1.1e-17 0.44 -0.01 0.07 1.1e-17 0.18 0.16 0.15 0.15 0.15 0.15 0.15 0.15 0.15 0.15	PDB	B CHAI	STAR		Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
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286 375 1.4e-19 0.13 0.07 P56LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P; GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL; NULL; NULL; KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO) YQPQPA; ILCK 14 CCHAIN: B; ILCK 15 TEGQ(PHOSPHO) YQPQPA; ILCK 14 CCHAIN: B; ILCK 15 TEGQ(PHOSPHO) YQPQPA; ILCK 14 CCHAIN: B; ILCK 15 TEGQ(PHOSPHO) YQPQPA; ILCK 14 CCHAIN: B; ILCK 15 TEGQ(PHOSPHO) YQPQPA; ILCK 14 CCHAIN: B; ILCK 15 TEGQ(PHOSPHOTYROSYL) PEPTIDE AC-PTYR-GLU-GLU-GLU-									CITAIN: B,	COMPAIN, COMPLEA 2 (PHOSPHOTRANSFERASE/PEPTIDE)
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A 242 379 6.4e-26 0.08 0.01 GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN:  NULL;  NULL;  RINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15 HUMAN P56 TYROSINE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU	-								P;	(PHOSPHOTRANSFERASE/PEPTIDE)
A 242 379 6.4e-26 0.08 0.01 P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQA; ILCK 14 CHAIN: B; ILCK 15 A 282 379 3.2e-21 0.49 0.15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU	l flus		281	377	1.1e-17	0.18	0.16		GROWTH FACTOR RECEPTOR	SH2 DOMAIN GRB2; GRB2, SH2
A         242         379         6.4e-26         0.08         0.01         P56==LCK== TYROSINE           KINASE; ILCK 7 CHAIN: A;         ILCK 8 TAIL PHOSPHOPEPTIDE           TEGQ(PHOSPHO)YQPQPA;         ILCK 14 CHAIN: B; ILCK 15           A         282         379         3.2e-21         0.49         0.15         HUMAN P56 TYROSINE           KINASE; ILKK 7 CHAIN: A;         ILKK 8 PHOSPHOTYROSYL           PEPTIDE AC-PTYR-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-CHAIN         PEPTIDE AC-PTYR-GLU-GLU-GLU-CHAIN									BOUND PROTEIN-2; CHAIN: NULL:	DOMAIN, PROTEIN NMR, SOLUTION STRUCTURES
A 282 379 3.2e-21 0.49 0.15 KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15 KINASE; ILKK 15 CHAIN: B; ILCK 15 KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE ACPTYR-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU	[왕		242	379	6.4e-26	0.08	0.01		P56==LCK== TYROSINE	COMPLEX (KINASE/PEPTIDE)
A 282 379 3.2e-21 0.49 0.15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-								_	KINASE; 1LCK 7 CHAIN: A;	,
A 282 379 3.2e-21 0.49 0.15 TEGQ(PHOSPHO)YQPQPA; ILCK 14 CHAIN: B; ILCK 15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-									1LCK 8 TAIL PHOSPHOPEPTIDE	
A 282 379 3.2e-21 0.49 0.15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-									TEGQ(PHOSPHO)YQPQPA;	
A 282 379 3.2e-21 0.49 0.15 HUMAN P56 TYROSINE KINASE; ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-	- [	1							1LCK 14 CHAIN: B; 1LCK 15	
	累		282	379	3.2e-21	0.49	0.15		HUMAN P56 TYROSINE	COMPLEX (TYROSINE
ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU-									KINASE; 1LKK 7 CHAIN: A;	KINASE/PEPTIDE)
PEVIIDE AC-PLYR-GLU-GLU-									ILKK 8 PHOSPHOTYROSYL	
		_							PEPTIDE AC-PTYR-GLU-GLU-	

PDB annotation				TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE, OXIDOREDUCTASE	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE,
Coumpound	12	PHOSPHOTRANSFERASE V-SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1SHA 3 RECOGNITION DOMAIN SH2) (E.C.2.7.1.112) COMPLEX WITH 1SHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 1SHA 5	SIGNALLING PROTEIN PHOSPHATIDYLINOSITOL 3- KINASE (E.C.2.7.1.137) (N- TERMINAL 2PNA 3 SH2 DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 STRUCTURES) 2PNA 4	SHP-2; CHAIN: A, B;	HCK SH2; CHAIN: NULL;	CHLOROPEROXIDASE L; CHAIN: A, B, C;	CHLOROPEROXIDASE L; CHAIN: A, B, C;
SEQFOL D score						85.13	
PMF score		0.07	0.78	0.04	0.25		1.00
Verify score		0.51	0.33	-0.31	0.19		0.36
Psi Blast		1.6e-24	6.4e-18	3.2e-27	1.6e-22	3e-41	3e-41
END AA		380	383	439	379	357	356
STAR T AA		284	286	257	281	92	84
CHAI N ID		A		A		A	Ą
PDB ID		1sha	2pna	2shp	3hck	1a88	1a88
SEQ ID NO:		1709	1709	1709	1709	1710	1710

PDB annotation	OXIDOREDUCTASE	HALOPEROXIDASE CHI OROPEROXIDASE A1	HALOPEROXIDASE A1;	HALOPEROXIDASE,	OXIDOREDUCTASE	HALOPEROXIDASE	HALOPEROXIDASE F;	HALOPEROXIDASE,	OXIDOREDUCTASE, PROPIONATE	TIAL OPEROXIES OF	HALOPEROXIDASE HALOPEROXIDASE	HALOPEROXIDASE	OXIDOREDUCTASE, PROPIONATE	COMPLEX	AMINOPEPTIDASE	AMINOPEPTIDASE, PROLINE	IMINOPEPTIDASE, SERINE	PROTEASE, 2 XANTHOMONAS	CAMPESTRIS	HYDROLASE HYDROLASE,	HALOALKANE DEHALOGENASE,	ALPHA/BETA-HYDROLASE	HYDROLASE HYDROLASE,	HALOALKANE DEHALOGENASE,	ALPHA/BETA-HYDROLASE	HALOPEROXIDASE	HALOPEROXIDASE A2,	CHLOROPEROXIDASE A2;	HALOPEROXIDASE,	OXIDOREDUCTASE, PEROXIDASE,	ALPHA/BETA 2 HYDROLASE FOLD, MUTANT M99T
Coumpound		BROMOPEROXIDASE A1;				CHLOROPEROXIDASE F;	CHAIN: NULL;			CIT OB OBEBOATD A CT. F.	CHAIN: NIII.:				PROLINE IMINOPEPTIDASE;	CHAIN: A, B;				HALOALKANE	DEHALOGENASE; CHAIN:	NULL;	HALOALKANE	DEHALOGENASE; CHAIN:	NULL;	BROMOPEROXIDASE A2;	CHAIN: NULL;				
SEQFOL D score		95.47				83.84									67.83				i	94.11						98.68					ĺ
PMF score										1 00	20.1												1.00								
Verify										0.61	70.0											-	0.45			,					
Psi Blast		8e-31				9e-41				00-41	1				1.5e-36					3e-43	-	,	3e-43			8e-32		_			
END AA		360				357				356	2				355					357		, ,	356		1	357					
STAR T AA		78				78				78	5				63					44		6	83			76					
CHAI N ID															Ą														•		
PDB ID		1a8q				1a8s				1980					1azw					1b6g		1	<b>3</b> 001			Ibrt	•				
SEQ ID NO:		1710				1710				1710	2				1710					1710		,	1/10			1710				_	

	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation .
	en	N ID	TAA	AA		score	score	D score		
' '	1c4x	А	72	357	3.2e-36			77.34	2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION
	1cqw	A	29	360	9e-47			122.01	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
	1cqw	Ä	74	358	9e-47	0.58	1.00	-	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
	1cv2	А	73	358	3e-44	0.60	1.00		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA- HYDROLASE
	lcvi		101	199	3 <b>e-1</b> 3	0.11	0.63		TRIACYLGL YCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
	lcvi		97	212	4.8e-09	0.25	0.07		TRIACYLGLYCEROL HYDROLASE; CHAIN: NULL;	HYDROLASE TRIACYLGLYCEROL- HYDROLASE, X-RAY CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE
	1ehy	∢	99	356	9.6e-37			119.90	SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN
	leki	A	62	356	8e-43	0.52	1.00		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR

Coumpound PDB annotation	_	EPOXIDE HYDROLÁSE; CHAIN: HYDROLÁSE HOMODIMER, A, B; DISUBSTITUTED UREA 2 INHIBITOR	EPOXIDE HYDROLASE; CHAIN: HYDROLASE HOMODIMER, A, B;	EPOXIDE HYDROLASE; CHAIN: HYDROLASE HOMODIMER,	ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	LIPASE, GASTRIC; CHAIN: A, B;   HYDROLASE LIPASE	PARA-NITROBENZYL HYDROLASE PNB ESTERASE; ESTERASE; CHAIN: A; ALPHA-BETA HYDROLASE	TRIACVI GI VCEROI HAVDROI ASE	. Ď;	TRIACYLGLYCEROL   PEPTIDE, CLOSED	HYDROLASE; CHAIN: E; CONFORMATION, 2 HYDROLASE,		Ö.		HYDROLASE; CHAIN: E;   CONFORMATION, 2 HYDROLASE,	EPOXIDE HYDROLASE: CHAIN:   EPOXIDE HYDROLASE EH:		 MINOPEPTIDASE;		PROLYL AMINOPEPTIDASE, 2	SERRATIA, IMINOPEPTIDASE	TRIACVI GIVCEROL - I IDASE I IDASE I IDASE	 E
JC		EPOXIDI A, B;	EPOXIDI A, B;	EPOXIDE	A, B;	LIPASE,	PARA-NI ESTERA	TRIACVI	HYDROL	TRIACYI	HYDROL	TRIACYI	HYDROL	TRIACYI	HYDROL	EPOXIDE	A, B;	PROLYL	CHAIN: A;			TRIACYI	וסמתעגנו
SEQFOL	D score										-	_						80.11					
PMF	score	1.00	1.00	1.00		0.07	0.27	0.81	( ) }			0.28				1.00						0.11	
Verify	score	0.56	0.58	69.0		0.13	0.76	0.38				0.37				0.46						0.10	
Psi Blast		1.2e-54	8e-43	3e-56		1.5e-06	4.5e-05	68-25	ì			4.8e-09				1.5e-45		6.4e-29				4.8e-10	
END	AA	356	356	356		226	215	238	 			212				358		360				215	
STAR	T AA	70	29	69		86	85	65				26				74		29				97	
CHAI	N IB	Ą	В	В		Ą	Ą	<u>ر</u>				Ω		_		A		Ą				О	
PDB	8	1ek1	lek1	lek1		lhlg	1qe3	100e	5			1dge				1qo7		1qtr				4lip	
SEQ	e ë	1710	1710	1710		1710	1710	1710				1710				1710		1710				1710	_

PDB annotation	ANALOGUE, ENANTIOSELECTIVITY			METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER
Coumpound		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MAT1; CHAIN: A;	RAG1; CHAIN: NULL;	RAGI; CHAIN: NULL;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;
SEQFOL D score								
PMF score		0.84	0.71	0.00	0.74	0.64	0.12	0.88
Verify score		-0.31	-0.18	-0.64	-0.02	-0.00	0.16	0.52
Psi Blast		6e-17	3.2e-14	4.5e-14	36-11	1.3e-07	0.009	1.4e-28
END AA		328	332	321	328	331	297	307
STAR T AA		275	278	276	272	280	194	171
CHAI N ID				A			A	₹.
PDB ID		1chc	1chc	1g25	1rmd	lrmd	lcrz	lerj
SEQ ID NO:		1711	1711	1711	1711	1711	1712	1712

PDB annotation	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE,
Coumpound	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	MJ0882; CHAIN: A;	CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;
SEQFOL D score			63.92			
PMF	96.0	1.00		1.00	0.43	0:30
Verify score	0.33	0.43		0.54	-0.10	-0.07
Psi Blast	1.3e-44	6.4e-39	1.6e-48	1.6e-48	6.4e-10	7.5e-11
END	289	290	307	305	446	455
STAR T AA	37	14	1	58	338	334
CHAI N ID	Ą	Я	В	В	A	
PDB ID	lerj	1got	lgot	lgot	1dus	lvid
SEQ ID NO:	1712	1712	1712	1712	1713	1713

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
1719	1040	Y	345	497	3.2e-13	0.14	0.53		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1719	1c40	A	371	494	4.5e-16	0.50	96.0		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN
1719	1cu1	A	20	170	0.0006	0.42	0.77		PROTEASE/HELICASE NS3; CHAIN: A, B;	HYDROLASE HEPATITIS C VIRUS, BIFUNCTIONAL, PROTEASE- HELICASE
1719	1d2m	A	345	497	3.2e-13	60.0	0.62		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1719	1d2m	¥	370	513	1.5e-16	-0.11	98.0		EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	HYDROLASE UVRB; MULTIDOMAIN PROTEIN
1719	1d9x	A	346	525	3e-20	0.35	66.0		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1719	149x	A	354	508	3.2e-18	0.20	0.43		EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	GENE REGULATION APO PROTEIN
1719	1fuk	А	338	208	1.1e-39	0.07	0.18		EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN
1719	1fuu	A	2	169	1.6e-25	0.02	0.35		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF44, HELICASE, DEAD-BOX PROTEIN
1719	1fuu	В	119	508	0	0.04	-0.06		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN
1719	1fuu	В	2	169	1.6e-25	90.0	0.21		YEAST INITIATION FACTOR	TRANSLATION EUKARYOTIC

PDB CHAI STAR END ID NID TAA AA	STAR T AA	END		Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
								4A; CHAIN: A, B;	INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
Ihei A 13 170 0.0	170		0.	0.0014	0.29	0.22		HCV HELICASE; CHAIN: A, B;	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE
1qde A 2 169 3.2.	169		3.20	3.2e-23	0.10	0.39	•	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	GENE REGULATION EIF44; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMILY
2pjr A 2 82 0.0006	83		0.0	900	0.22	0.33		HELICASE PCRA; CHAIN: A, F; HELICASE PCRA; CHAIN: B, G; DNA (S'-D(*TP*TP*TP*TP*T)-3'); CHAIN: C, D; DNA (S'-D(*GP*C)-3'); CHAIN: H; DNA (S'- D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1aox A 28 170 1.1e-21	170		1.1e-	-21	0.62	1.00		INTEGRIN ALPHA 2 BETA; CHAIN: A R:	INTEGRIN INTEGRIN, CELL APHESION GI YCOPPOTEIN
laox         A         28         220         1.1e-21	220		1.1e-	21			75.90	INTEGRIN ALPHA 2 BETA; CHAIN: A. B:	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
latz A 31 213 4.8e-17	213		4.8e-	17			89.44	VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN- BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
lauq 23 221 1.6e-26	221		1.6e-	26			65.12	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL:	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
lauq 30 220 1.6e-26	220		1.6e-	56	0.79	66.0		AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL:	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1bpv 211 302 3.2e-1	302		3.2e	=	0.22	-0.01		TITIN; CHAIN; NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1bpv 329 427 9e-12	427		9e-1	2	0.65	0.41		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN

		,																
PDB annotation	TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN											STRUCTURAL PROTEIN I-DOMAIN,	METAL BINDING, COLLAGEN, ADHESION	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN,	ADHESION	
Coumpound		TITIN; CHAIN: NULL;	GP130; CHAIN: A, B;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO	AMINO PROXIMAL	REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	NEURAL ADHESION MOLECULE DROSOPHILA	NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT CONTAINING THE LCFR 3 TWO	AMINO PROXIMAL	FIBRONECTIN TYPE III	KEFEA1S ICFB 4 (KESIDUES 610 - 814)) 1CFB 5	INTEGRIN ALPHA-1; CHAIN: A,	H;	INTEGRIN ALPHA-1; CHAIN: A, B;		CELL ADHESION PROTEIN
SEQFOL D score				52.60														
PMF score		0.09	0.48					-0.07						1.00		1.00		0.72
Verify score		0.47	0.45					60.0						0.46		96.0		0.49
Psi Blast		3.2e-13	3.2e-12	1.4e-11		4		1.4e-11						9.6e-21		6e-38		1.1e-13
END		418	419	427				412						170		209		415
STAR T AA		342	337	208				209						33		34		338
CHAI N ID		,	Ą											A		A		-
PDB ID		1bpv	15qu	1cfb				1cfb						1ck4		1ck4		1fna
SEQ ID		1721	1721	1721				1721						1721		1721		1721

PDB CHA	CHA	ٔ دا	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
<u> </u>		N I	TAA	AA		score	score	D score		
									FIBRONECTIN CELL. ADHESION MODULE TYPE III- 10 IFNA 3	
1fnf			106	444	1.4e-26	-0.05	0.13		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1fnf			27	415	1.6e-31	-0.00	-0.06		FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLILAR MATRIX 18NF 18
1fnf			28	425	1.6e-31			91.50	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1fnh		A	107	421	1.6e-24	0.16	-0.09		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1fnh		A	133	421	1.1e-26			73.33	FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1fnh		A	213	445	1.1e-26	-0.04	0.49		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING
1fns		Ą	30	217	1.6e-25	0.97	1.00		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H: VON	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX
									WILLEBRAND FACTOR; CHAIN: A;	(WILLEBRAND/IMMUNOGLOBULIN ), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
lido			32	208	7.5e-37			91.05	INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX. CYTOSKELETON
lido			34	206	7.5e-37	0.65	1.00		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
11fa		A	33	213	1.5e-36			78.17	CD11A; ILFA 5 CHAIN: A, B; 1LFA 6	CELL ADHESION LFA-1, ALPHA- L',BETA-2 INTEGRIN, A-DOMAIN;

PDB annotation	1LFA 8	CELL ADHESION LFA-1, ALPHA- L\BETA-2 INTEGRIN, A-DOMAIN; 1LFA 8	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION INTEGRIN, CELL ADHESION	CELL ADHESION INTEGRIN, CELL ADHESION	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
Coumpound		CD11A; 1LFA 5 CHAIN: A, B; 1LFA 6	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;
SEQFOL D score			75.51						
PMF score		1.00		0.58	0.37	1.00	1.00	-0.07	0.72
Verify score		99.0		0.08	0.42	0.55	66'0	0.05	0.04
Psi Blast		1.5e-36	6.4e-24	6.4e-24	8e-17	8e-21	7.5e-28	1.6e-18	1.6e-22
END AA		209	425	415	445	170	209	419	421
STAR T AA		34	211	215	342	30	34	214	214
CHAI N ID		А				Ą	A	Ą	A
PDB ID		11fa	lmfn	1mfn	lmfn	19c5	19c5	1923	1qr4
SEQ ID NO:		1721	1721	1721	1721	1721	1721	1721	1721

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PDB annotation	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN				PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	COAGULATION FACTOR	
Coumpound	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	HORMONE/RECEPTOR HUMÁN GROWTH HORMONE COMPI EXED WITH ITS
SEQFOL D score	77.31								
PMF score		0.34	66.0	0.81	0.70	0.84	0.86	-0.17	-0.19
Verify score		0.55	0.06	0.92	0.27	0.55	0.71	80.0	80.0
Psi Blast	1.6e-22	1.4e-13	3e-12	1.2e-13	3.2e-14	1.3e-06	3.2e-11	1.1e-12	1.5e-16
END	421	445	301	421	415	281	421	416	422
STAR T AA	214	337	210	335	337	215	337	215	215
CHAI N ID	Ą	A				A	A		В
PDB ID	1qr4	1qr4	Iten .	Iten	1ttf	2fnb	2fnb	2hft	3hhr
SEQ ID NO:	1721	1721	1721	1721	1721	1721	1721	1721	1721

PDB annotation		TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN		COMPLEX (KINASE/INHIBITOR)
Coumpound	RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE; CHAIN: NULL;	TRANSFERASE(PHOSPHOTRA NSFERASE) \$C-/AMP\$- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6 TRANSFERASE(PHOSPHOTRA NSFERASE) \$C-/AMP\$- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE	DETERGENT MEGA-8 1APM 6 CYCLIN-DEPENDENT KINASE
SEQFOL D score				59.46	52.92
PMF		0.58	0.27	0.88	
Verify score		0.19	-0.31	-0.22	
Psi Blast		4.5e-06	4.8e-39	3.2e-47 3.2e-47	8e-24
END AA		236	355	356	355
STAR T AA		146	147	143	104
CHAI N ID		В		ш	A
PDB ID		1fuu	1a06	lapm lapm	1bi8
SEQ ID NO:		1723	1724	1724	1724

PDB annotation	CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX					TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
Coumpound	6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) 1CMK 4	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	TRANSFERASE (PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	P38 MAP KINASE; CHAIN: NULL;
SEQFOL D score			59.27		58.35		56.49
PMF score		0.70		0.77		0.54	,
Verify score		-0.22		-0.14		0.07	
Psi Blast		1,6e-48	1.6e-48	1.6e-48	1.6e-48	4.8e-36	1.1e-18
END		356	413	356	399	361	401
STAR T AA		143	69	143	77	147	1.1
CHAI N ID		щ	豆	ш	ъ	ပ	
PDB.		lcmk	1cmk	1ctp	1ctp	1f3m	lian
SEQ ID NO:		1724	1724	1724	1724	1724	1724

PDB annotation	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING,	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION	AMINE/CARBOXYLATE LIGASE AMINE/CARBOXYLATE LIGASE	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP-RIBONUCLEOPROTEIN	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
	KINASE K INTRASTE	KINASE K INTRASTE	TRANSFERASI ACTIVATED P TRANSFERASI SERINE/THRE KINASE, 2 P38	KINASE RABBIT PHOSPHORYLAV GLYCOGEN ME' TRANSFERASE, SERINE/THREOD KINASE, ATP-BI	TRANSFE SERINE/TJ KINASE, T	TRANSFE SERINE/TI KINASE, 1	SERINE K TITIN, MU	AMINE/C/ AMINE/C/	COMPLEX PROTEIN/ (NUCLEAI	RNA-BÍNI PRE-MRN
Coumpound	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NULL;	PHOSPHORYLASE KINASE; CHAIN: NULL;	ERK2; CHAIN: NULL;	ERK2; CHAIN: NULL;	TITIN; CHAIN: A, B;	GLUTATHIONE SYNTHETASE; CHAIN: A;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-
SEQFOL D score			60.82			58.82				
PMF score	0.11	0.55		0.81	0.13		0.54	0.52	0.52	0.95
Verify score	-0.27	-0.31		0.03	-0.10		-0.27	-0.23	0.40	0.26
Psi Blast	1.1e-33	6.4e-34	1.6e-24	3.2e-43	1.1e-24	1.1e-24	3.2e-27	0.0088	7.5e-07	9e-05
END	356	356	403	356	414	392	362	99	953	616
STAR T AA	148	150	42	127	162	83	150	m	886	542
CHAI N ID		A					Ą	A	В	А
PDB ID	1koa	1kob	1p38	1phk	1pme	1pme	1tki	2hgs	la9n	1b7f
SEQ ID NO:	1724	1724	1724	1724	1724	1724	1724	1726	1728	1728

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PDB annotation	REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	GENE REGULÁTION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULÁTION/RNÁ	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	RNA BINDING PROTEIN/RNA NESTED DOUBLE PSEUDOKNOT RNA STRUCTURE	RNA BINDING PROTEIN RNA- BINDING DOMAIN
Coumpound	R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	ALPHA SPECTRIN; CHAIN: A, B, C;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP;); CHAIN: M, N, O, P, Q, R, S, T;	UIA PROTEIN; CHAIN: A; HDV RIBOZYME SELF-CLEAVED; CHAIN: B;	HU ANTIGEN C; CHAIN: A;
SEQFOL D score								
PMF score		0.43	0.10	1.00	0.57	0.43	0.53	0.53
Verify score		0.08	-0.04	-0.10	0.47	0.54	-0.15	0.64
Psi Blast		3e-07	0.003	4.5e-05	7.5e-07	7.5e-07	6e-05	1.5e-05
END AA		958	835	612	956	950	614	614
STAR T AA		688	720	544	688	887	540	540
CHAI N ID		A	A	¥	Ą	Ŧ.	A	A
PDB ID		167f	1cun	1cvj	levj	1cvj	1cx0	1d8z
SEQ ID NO:		1728	1728	1728	1728	1728	1728	1728

PDB annotation		RNA BINDING PROTEIN RNA- BINDING DOMAIN	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX: MILTI-STIBLINIT	RIBONUCLEOPROTEIN UIA117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN		RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
Coumpound		HU ANTIGEN C; CHAIN: A;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B:	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEOLIN RBD1; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES I - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POL YPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;
SEQFOL	D score			:		,			
PMF	score	08'0	0.37	99.0	0.21	. 66.0	0.71	66.0	0.22
Verify	score	0.48	-0.23	0.65	0.48	0.42	0.32	0.13	-0.14
Psi Blast		3e-0 <i>5</i>	3e-06	1.5e-05	6e-07	1.5e-05	6e-07	10-08	7.5e-05
END	AA	865	835	614	947	612	614	946	614
STAR	TAA	542	709	540	887	541	560	988	493
CHAI	OI N	A	В		A		А	В	A
PDB	a l	1 <b>d</b> 9a	1dn1	1fht	1£37	Tha T	1hd1	lnrc	1qm9
SEQ	NO.	1728	1728	1728	1728	1728	1728	1728	1728

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RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION		COMPLEX (RIBONUCLEOPROTEIN/RNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA),
POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	UIA SPLICEOSOMAL PROTEIN; IURN 5 CHAIN: A, B, C; IURN 6 RNA 21MER HAIRPIN (5'- (AP*AP*UP*CP*CP*AP*UP*UP* IURN 11 CHAIN: P, Q, R IURN 13	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED
0.10	0.82	0.40	0.03	0.75	0.39	0.43	0.75
0.10	0.51	-0.03	-0.03	0.18	0.42	0.05	0.51
1.5e-07	0.0001	0.0001	1e-06	4.5e-06	3e-05	6e-07	7.5e-07
947	610	619	614	614	616	946	612
828	540	540	560	542	542	887	525
∀		A	A				A
Iqm9	1sxl	lurn	2mss	2sx1	2u1a	2u1a	2up1
1728	1728	1728	1728	1728	1728	1728	1728
	Iqm9         A         828         947         1.5e-07         0.10         0.10         POLYPYRIMIDINE TRACT-BING PROTEIN; CHAIN: A;	Iqm9         A         828         947         1.5e-07         0.10         0.10         POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;           IsxI         540         610         0.0001         0.51         0.82         LETHAL PROTEIN (C-TERMINUS, OR SECOND RNA-BINDING DOMAIN ISXL 3 (RBD-2), RESIDUES 199-294           PLUS N-TERMINAL MET) ISXL         4 (NMR, 17 STRUCTURES) ISXL         4 (NMR, 17 STRUCTURES) ISXL	19m9   A   828   947   1.5e-07   0.10   0.10   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;   1.5e-07   0.10   0.10   BINDING PROTEIN; CHAIN: A;   1.5m   14m9   A   828   947   1.5e-07   0.10   0.10   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;   15m   1   1   1   1   1   1   1   1   1	14m9   A   828   947   1.5e-07   0.10   0.10   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;   1540   610   0.0001   0.51   0.82   ETHAL PROTEIN (C-TETMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINUS, OR SECOND RNA-BINDING DOMAIN 1SXL 3   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 5   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 1   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 1   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1SXL 1   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL MET) 1   (RBD-2), RESIDUES 199 - 294   PLUS N-TERMINAL PROTEIN; CHAIN: A; RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2, RDD-2,	19m9   A   828   947   1.55-07   0.10   0.10   POLYPYRIMIDINE TRACT-BINDING PROTEIN; CHAIN: A;   1.56-07   0.100   0.51   0.82   RNA-BINDING PROTEIN SEX-LETHAL PROTEIN (C-TERMINUS, OR SECOND-RNA-BINDING DOMAIN 1SXL 3   RBD-2), RESIDUES 199-294   RDD-STANDING PROTEIN SEX-STANDING DOMAIN 1SXL 3   RBD-2), RESIDUES 199-294   RDD-STANDING PROTEIN; CHAIN: A   540   619   0.0001   -0.03   0.40   UIA SPLICEOSOMAL PROTEIN; CHAIN: A   S60   614   16-06   -0.03   0.40   UIA SPLICEOSOMAL PROTEIN; CHAIN: A   S60   614   16-06   -0.03   0.03   MUSASHII; CHAIN: A; RBD-STANDING PROTEIN; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; CHAIN: NULL; 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PDB annotation	HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA),	RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION	KNA BINDING DOMAIN KNA BINDING DOMAIN, RBD, RNA	KECOGINITION MOTIF, KKM, Z   SPLICING INHIBITOR.	TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION. X CHROMOSOME	DOSAGE COMPENSATION	PLASMA PROTEIN PLASMA PROTEIN, METAL-BINDING, LIPID- RINDING						
Coumpound	TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED	IELUMEIKIC DINA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;			C S . THE STATE OF THE PARTY STATES	SEA-LEITAL; CHAIN; A, B, C;				SERUM ALBUMIN; CHAIN: A;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 1AHD 3	REPLACED BY SER (C39S)	1AHD 4 16 STRUCTURES) 1AHD
SEQFOL D score									<del></del>									
PMF score		0.95		1.00			9,0	0.40				0.17		0.18				
Verify score		0.32		0.58			0,00	0.30				-0.27		-0.46			***	
Psi Blast		7.5e-07		1e-05				70-95				0.0015		1.1e-28				
END AA		947		612			0.50	076				336		347				
STAR T AA		688		542			000	600				661		267				
CHAI N ID		4		∢				¢				Ą		Ъ				
PDB ID		2up1		3sxl			2000	TVeC				le7f		lahd				
SEQ ID NO:		1728		1728			1700	07/1				1730		1733				

T	1"	1		1	1			
	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION				
5	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) 1LFB 3	GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA- BINDING IPRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) IPRA 4	GENE REGULATING PROTEIN REPRESSOR (AMINO- TERMINAL DOMAIN) (R1-69) 1R69 4	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT
	0.07	0.46	0.92	1.00	0.99	0.51	0.78	0.19
	-0.02	-0.12	-0.04	0.38	0.61	0.08	0.15	60'0
	6.4e-24	6.4e-24	3.2e-23	9.6e-22	6e-24	0.00015	0.0003	1.6e-26
	343	340	341	339	336	205	205	347
	271	270	266	267	271	173	173	273
	A	A	A	В				
	1b72	168i	161	161	11fb	1pra	1r69	lsan
	1733	1733	1733	1733	1733	1733	1733	1733
	50	1b72 A 271 343 6.4e-24 -0.02 0.07 HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: B; DNA CHAIN: E;	1b72 A 271 343 6.4e-24 -0.02 0.07 HOMEOBOX PROTEIN HOX-BI; I CHAIN: A; PBXI; CEANN: B; DNA CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D; CHAIN: D; CHAIN: D; CHAIN: D; CHAIN: D; CHAIN: D; CHAIN: D;	1672 A   271   343   6.4e-24   -0.02   0.07   HOMEOBOX PROTEIN HOX-BI;   168i   A   270   340   6.4e-24   -0.12   0.46   ULTRABITHORAX HOMEOTIC   PROTEIN IV; CHAIN: B;   168i   A   270   340   6.4e-24   -0.12   0.46   ULTRABITHORAX HOMEOTIC   PROTEIN IV; CHAIN: B;   168i   A   266   341   3.2e-23   -0.04   0.92   C.; DNA; CHAIN: D, E, F   168i   A   266   341   3.2e-23   -0.04   0.92   C.; DNA; CHAIN: D, E, F   168i   A   266   341   3.2e-23   -0.04   0.92   C.; DNA; CHAIN: D, E, F   168i   C.; DNA; CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: D, E, F   168i   C.; DNA; CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN: C, CHAIN:	1b72   A   271   343   6.4e-24   -0.02   0.07   HOMEOBOX PROTEIN HOX-BI;   CHAIN: A; PBXI; CHAIN: B;   DNA CHAIN: D; DNA CHAIN: B;   DNA CHAIN: D; DNA CHAIN: B;   DNA CHAIN: B;   DNA CHAIN: B;   DNA CHAIN: B;   DNA CHAIN: A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   HOMEOBOX PROTEIN   A;   DNA (5'-CHAIN: C)   D	1b72   A   271   343   6.4e-24   -0.02   0.07   HOMEOBOX PROTEIN HOX-BI;     1b8i   A   270   340   6.4e-24   -0.12   0.46   ULTRABITHORAX HOMEOTIC PROTEIN IN; CHAIN: B;     1b8i   A   270   340   6.4e-24   -0.12   0.46   ULTRABITHORAX HOMEOTIC PROTEIN IN; CHAIN: B;     1fi   A   266   341   3.2e-23   -0.04   0.92   PAIRED PROTEIN; CHAIN: B;     1fi   B   267   339   9.6e-22   0.38   1.00   PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F     1fi   B   271   336   6e-24   0.61   0.99   TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR ITERIT (HOMEODOMAIN) 1LFB 3	1b72	1672 A   271   343   64e-24   -0.02   0.07   CHAIN: 4; PBXI; CHAIN: B; DIA CHAIN: B; DIA CHAIN: B; DIA CHAIN: B; DIA CHAIN: B; DIA CHAIN: B; DIA CHAIN: CHAIN: B; DIA CHAIN: CHAIN: B; DIA CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CHAIN: CH

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PDB annotation		TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)			PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING
Coumpound	WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	UL TRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F
SEQFOL D score									
PMF		0.17	0.29	0.04		0.18	0.07	0.28	0.92
Verify score		-0.16	-0.59	-0.27		-0.46	-0.02	-0.31	-0.04
Psi Blast		0.0003	0.0003	3.2e-26		1.6e-28	1.6e-24	8e-24	1.6e-23
END		205	205	341		347	343	340	341
STAR T AA		173	173	271		267	271	271	266
CHAI N ID				Ą		Ъ	A	A	A
PDB ID		1zug	2cro	9ant		1ahd	1b72	158i	1년1
SEQ ID NO:		1733	1733	1733		1734	1734	1734	1734

PDB annotation	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION					1					TRANSCRIPTION REGULATION	GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD;
Coumpound		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFBI (HOMEODOMAIN) ILFB 3	GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA- BINDING 1PRA 3 DOMAIN,	RESIDUES 1-69) (NMR, 20 STRUCTURES) IPRA 4	GENE REGULATING PROTEIN REPRESSOR (AMINO-	1ECMINAL DOMAIN) (KI-09)	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3	REPLACED BY SER AND	(C39S,DEL 1-6) ISAN 4 (NMR, 20	PHAGE 434 CRO PROTEIN;	CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C,
SEQFOL D score															
PMF score		1.00	66.0	0.51		0.78		61.0				0.17		0.29	0.04
Verify score		0.38	0.61	0.08		0.15		60.0				-0.16		-0.59	-0.27
Psi Blast		8e-22	6e-24	0.00015		0.0003		6.4c-26		***		0.0003		0.0003	8e-26
END AA		339	336	205		205		347				205		205	341
STAR T AA		267	271	173		173		273				173		173	271
CHAI N ID		В													A
PDB ID		161	11fb	1pra		1r69		lsan				1zug		2cro	9ant
SEQ ID NO:		1734	1734	1734		1734		1734				1734		1734	1734

STAR         END         Psi Blast         Verify         PMF         SEQFOL         Coumpound           T AA         AA         score         b score         D score         D, E, F;           1         101         4.8e-30         -0.11         0.06         TROPONIN C; CHAIN: NULL;
23 170 1.4e-38 82.97 TROPONIN C; CHAIN: NULL;
25 169 1.4e-38 0.17 0.70 TROPONIN C; CHAIN: NULL;
30 104 1.1e-29 75.36 CALMODULIN; CHAIN: NULL;
22 109 6.4e-23 61.36 CARDIAC N-TROPONIN C; CHAIN: NULL;
1 101 3.2e-20 0.08 -0.01 SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;
26 106 3.2e-26 70.90 TROPONIN C; CHAIN: A, B;
20 109 8e-27 71.63 N-TROPONIN C; CHAIN: NULL;
33 170 4.8e-34 S7.30 MYOSIN; CHAIN: A, B, C, D, E,

		_																			_		_								_
PDB annotation		PROTEIN	CALCIUM BINDING CALCIUM BINDING																										CALCIUM-BINDING PROTEIN	CALMODOLIN APO 1K2C-DOMAIN; 1CMF 9	STRIPLICATION I DE CATETAL LIEU IV
Coumpound		F, G, H;	CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN	CALMODOLLIN COMPLEXED	WITH CALMODOLIN-BINDING	CALMODIII IN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	1CLL 3	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	ICLL 3	CALMODULIN (VERTEBRATE);	ICMF & CHAIN: NOLL; ICMF /	CARDIAC TROPONTM C.
SEQFOL	D score		50.72						85.63	٠																89.82			68.52		
PMF	score			0.82		_						•			0.92						0.40		0.81								800
Verify	score			0.01											80.0						. 60.0		-0.02								000
Psi Blast			3.2e-11	8e-35		-			1.4e-47				•		1.4e-47						3.2e-35		9.6e-53			9.6e-53			7.5e-23		4.8e-29
END	AA		103	102					158						169						102		169			170			104		101
STAR	1 AA		2	-					33						33						_		33			33			33		
CHAI				Ą					A						Ą																Ą
PDB	3		1bu3	lcdm					1cdm						1cdm						-   3		Icli			lcll			lcmf		1dtl
SEQ	NO:		1738	1738					1738		***************************************				1738						1738		1738			1738			1738		1738

PDB annotation		TURN-HELIX	STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER						CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	REGULATED 3 MUSCLE	COINTRACTION	CALCIUM-REGULATED MUSCLE	CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	REGULATED 3 MUSCLE	CONTRACTION	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE
Coumpound		CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	CALCIUM BINDING PARVALBUMIN (PIKE, PI 5.0, A1 PHA COMPONENT:	COMPLEXED WITH IPVAA 1	TWO CALCIUM IONS	DIFFRACTION) IPVAA 2	CALCIUM-BINDING PROTEIN ALPHA-PARVALBUMIN 1RTP 3	TROPONIN C; CHAIN: NULL;						TD OD ONINI O. CHIANA SHITT	IROPONIN C; CHAIN: NULL;							TROPONIN C; CHAIN: NULL;
SEQFOL	D score					55.26				55.44							27.00	89.65							
PMF	score		0.72	0.80	0.89						0.35														96.0
Verify	score		0.26	-0.11	0.03						-0.10														-0.13
Psi Blast			9.6e-36	3.2e-34	4.8e-51	1.6e-15				3.2e-16	1.1e-30						16.41	1,06-41							1.6e-41
END	AA		169	101	169	104				104	101						160	601							169
STAR	TAA		31	1	31	7				L	1						7.0	<del>+</del> 7							33
CHAI	A .		A	A	A	A				1										_					
PDB	<b>a</b>		1dt[	lexr	lexr	1pva				lrtp	1tcf						140£	1311			,				Itcf
SEQ	e ö		1738	1738	1738	1738				1738	1738						1720	1/30							1738

PDB annotation	CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION	REGULATED 3 MUSCLE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14	CALCIUM-BINDING PROTEIN BF- HAND 1TNX 14	CALCIUM-BINDING PROTEIN EF- HAND 1TNX 14						CALMODULM, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2
Coumpound			TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCTUM BINDING PROTEIN CALMODULIN (/TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score				84.53			96.98		62.97	66.58		60.06
PMF			0.41		0.94	0.30		1.00			0.36	
Verify			-0.26		0.17	-0.20		0.13			-0.06	
Psi Blast			9.6e-34	1.6e-38	1.6e-38	3.2e-32	4.8e-42	4.8e-42	.8e-22	3.2e-26	9.6e-36	1.1e-51
END			101	169	169	101	169	169	103	106	104	170
STAR T AA			-	24	33		20	33	36	31	-	31
CHAI N ID					,				Y		A	А
PDB ID			1tmx	1tmx	1tmx	ltop	1top	1top	1trc	1trf	lvrk	1vrk
SEQ ID NO:			1738	1738	1738	1738	1738	1738	1738	1738	1738	1738

PDB CHAI STAR E	STAR	<b>-</b>	2	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
OI N	TAA		-		score	score	D score		
									COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1vrk A 33 169 1.1e-51	169 1.16	1.1e	1.1e-51		0.15	0.95		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1wdc B 33 170 7.5e-26	170		7.5e-26				64.97	SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
lwdc C 33 171 1.1e-25	171		1.1e-25				54.16	SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
3ctn 31 104 8e-10	104		8e-10				52.43	TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
4cpv 6 103 1.3e-11	103		1.3e-11	<u></u>			51.70	CALCIUM BINDING CALCIUM- BINDING PARVALBUMIN (\$P*I=4.25) 4CPV 3	
1ukz 362 463 0.0006 -	463 0.0006	463 0.0006		1	-0.05	0.07		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 1UKZ 3	
12ak A 362 587 0.0001	587 0.0001	587 0.0001		<u>'</u>	-0.17	0.13		ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE ATP:AMP- PHOSPHOTRANSFERASE, TRANSFERASE
3adk 362 495 0.0075	495 0.0075	495 0.0075	7.5		-0.25	0.16		TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
lukz 362 463 0.0006	463 0.0006	463 0.0006	9(		-0.05	0.07		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 1UKZ 3	

PDB annotation	TRANSFERASE ATP: AMP-PHOSPHOTRANSFERASE, TRANSFERASE		TRANSFERASE BRUTON'S AGAMMAGLOBULINEMIA TYROSINE KINASE, BTK; TRANSFERASE, PH DOMAIN, BTK MOTIF, ZINC BINDING, X-LINKED 2 AGAMMAGLOBULINEMIA, TYROSINE-PROTEIN KINASE	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPPI, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	HYDROLASE METALLO-BETA- LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE
Coumpound	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	BRUTON'S TYROSINE KINASE; CHAIN: A, B;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	GRP1; CHAIN: A;	PENICILLINASE; CHAIN: A;
SEQFOL D score							
PMF score	0.13	0.16	0.04	0.83	0.99	0.75	-0.14
Verify score	-0.17	-0.25	-0.50	0.14	0.25	-0.02	0.08
Psi Blast	0.0001	0.0075	90-99	3e-15	3e-16	7.5e-12	1.6e-14
END AA	587	495	142	142	142	142	178
STAR T AA	362	362	53	55	48	52	E.
CHAI N ID	4		∢	∢	A	A	A
PDB ID	Izak	3adk	1btk	Ifao	1fb8	1fgy	Isml
SEQ ID NO:	1746	1746	1749	1749	1749	1749	1750

PDB annotation	HYDROLASE HYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL	HYDROLASE PHOSPHOLIPASE C; ZINC PHOSPHOLIPASE C, GANGRENE DETERMINANT, C2 DOMAIN, CA 2 AND MEMBRANE BINDING, HYDROLASE	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE, 15LO_DEPOT2	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE, 15LO DEPOT2	DIOXYGENASE L-1; DIOXYGENASE, LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS	DIOXYGENASE L-1; DIOXYGENASE, LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS
Coumpound	METALLO BETA-LACTAMASE II; CHAIN: A, B;	LIPOXYGENASE-3; CHAIN: NULL;	LIPOXYGENASE-3; CHAIN: NULL;	ALPHA-TOXIN; CHAIN: NULL;	TRIACYLGLYCEROL ACYL- HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	15-LIPOXYGENASE; CHAIN: NULL;	15-LIPOXYGENASE; CHAIN:   NULL;	LPOXYGENASE-1; CHAIN:   NULL;	LIPOXYGENASE-1; CHAIN: NULL;
SEQFOL D score	-	253.58					482.93	231.83	
PMF score	-0.05		1.00	0.04	0.45	1.00			1.00
Verify score	0.18		0.36	-0.01	0.46	0.41			0.18
Psi Blast	1.6e-14	0	0	1.6e-20	0.0045	0	0	. 0	0
END AA	170	711	711	111	66	711	711	711	711
STAR T AA	8		35	7	4	2	2	-	46
CHAI N ID	А				A	-			
PDB ID	2bc2	1byt	1byt	lca1	leth	11ox	llox	lyge	1yge
SEQ ID NO:	1750	1751	1751	1751	1751	1751	1751	1751	1751

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PDB annotation	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G- PROTEIN, SIGNALING PROTEIN	SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA; RHO GDI 1; RHO GTPASE, G- PROTEIN, SIGNALING PROTEIN	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY	CELL CYCLE CDC42; RHO GDI 1; GTP-BINDING PROTEIN, CDC42, RHOGDI, X-RAY			•	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
Coumpound	TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP DISSOCIATION INHIBITOR ALPHA; CHAIN: E, F;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR 1; CHAIN: B;	GTP-BINDING PROTEIN; CHAIN: A; GDP-DISSOCIATION INHIBITOR I; CHAIN: B;		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;
SEQFOL D score						70.63		
PMF score	1.00	1.00	1.00	1.00			0.90	0.98
Verify score	0.50	0.33	0,48	0.48			-0.12	-0.15
Psi Blast	4.5e-66	9.6e-70	92-99	1.6e-78		6.4e-36	6.4e-36	3e-31
END	162	177	162	180		98	83	81
STAR T AA	24	24	ري د	S		. 61	50	21
CHAI N ID	m	ជា	В	В		<u>е</u>	24	Ą
PDB ID	1cc0	1cc0	1doa	1doa		lahd '	land	1b72
SEQ ID	NO: 1753	1753	1753	1753		1757	1757	1757

PDB annotation		PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,	HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	TRANSCRIPTION/DNA	ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,	HOMEOTIC PROTEINS,	DEVELORIMEINI, & SPECIFICII I										
Coumpound		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D: DNA CHAIN: F:	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN	EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D:	ULTRABITHORAX HOMEOTIC	PROTEIN IV; CHAIN: A; HOMEOBOX PROTEIN	EXTRADENTICLE; CHAIN: B;	CHAIN: D;	DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN)	12	PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) 1FTZ 3	DNA-BINDING PROTEIN OCT-1 (POU DOMAIN) 10CT 3	DNA-BINDING PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 1SAN 3	REPLACED BY SER AND	RESIDUES 1-6 DELETED   C39S DEL 1-6 1SAN 4 (NMR 20	STRUCTURES) ISAN 5
SEQFOL	D score		64.24	64.34						66.44				65.69					
PMF	score	66.0				0.82		•			0.81		0.23						
Verify	score	0.19				-0.14					-0.01		-0.70						
Psi Blast		3.2e-28	3e-31	6.4e-31		6.4e-31				4.8e-32	4.8e-32		3e-31	1.6e-33					
END	AA	81	81	77		78				98	85		79	98					
STAR	T AA	24	6	20		2				18	19		_	25					
CHAI	NID	∢	A	4		A							Ü						
PDB	a	1672	1672	lb8i		168i				lftz	1ftz		loct	Isan					
SEQ	NO E	1757	1757	1757		1757				1757	1757		. 1757	1757					

		.X (DNA-	X (DNA-		I NGAL; CALIN	БТА			EIN OBP SPORT, NDING 2
PDB annotation		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMBODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	LIPOCALIN LIPOCALIN, OLFACTION	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN	ALLERGEN LIPOCALIN, BETA BARREL			ODORANT-BINDING PROTEIN OBPOLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2
Coumpound	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ODORANT BINDING PROTEIN; CHAIN: A, B;	HUMAN NEUTROPHIL GELATINASE; CHAIN: A, B;	ALLERGEN EQU C 1; CHAIN: A;	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	ODORANT-BINDING PROTEIN; CHAIN: A, B;
SEQFOL D score			68.97					64.35	
PMF score	0.98	1.00		98.0	1.00	0.95	1.00		-0.02
Verify score	-0.17	-0.13		0.63	99.0	0.90	0.78		0.19
Psi Blast	1.66-33	1.6e-33	1.6e-33	3e-35	4.5e-47	1.4e-38	6e-37	6e-37	9e-36
END	82	79	79	169	169	691	168	891	172
STAR T AA	56	24	24	38	20	30	25	25	30
CHAI N ID		Ą	A	A	A	А			A
PDB UD	lsan	9ant	9ant	1a3y	1dfv	Iew3	1mup	dnwJ	10bp
SEQ ID	NO: 1757	1757	1757	1758	1758	1758	1758	1758	1758

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PDB annotation	PROTEIN	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL LIPOCALIN, SIGNAL PROTEIN, GLYCOPROTEIN		LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U. GLOBULIN, LIPID BINDING PROTEIN		COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB	LIGHT CHAIN, FAB HEAVY CHAIN	COMPLEX (VIKAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN. 2 P24	COMPLEX (MHC/VIRAL	PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-	CELL RECEPTOR, VIRAL PEPTIDE, 2	COMPLEX (MHC/VIRAL	PEPTIDE/RECEPTOR	IMMUNOGLOBULIN HUMAN FAB,	ANTI-TETANUS TOXOID, HIGH	AFFINITY, CRYSTAL Z FACKING MOTTE, PROGRAMMING
Coumpound		NEUTROPHIL GELATINASE; CHAIN: A;	RETINOL TRANSPORT RETINOL BINDING PROTEIN IRBP 3	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A. B: ANTIBODY FAB25.3	FRAGMENT; CHAIN: H, K, L, M;		HLA-A 0201; CHAIN: A; BETA-2	MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T	CELL RECEPTOR ALPHA;	CHAIN: D; T CELL RECEPTOR	BETA; CHAIN: E;	FAB B7-15A2; CHAIN: L, H;		
SEQFOL D score						78.30					295.76							
PMF score		1.00	-0.09	66.0	1.00			1.00								1.00		
Verify score		0.83	0.14	0.69	0.91			0.30								0.48		
Psi Blast		4.5e-40	1e-35	1.3e-36	1.5e-37	1.5e-37		1.6e-94			4.8e-64					1.6e-95		
END		169	168	169	169	691		249			263					252		
STAR T AA		17	26	25	25	25		21			22					22		
CHAI N ID		A		A	A	A		H			田					Ξ		
PDB ID		lqqs	1rbp	2a2u	2a2u	2a2u		Iafv			lao7					laqk	_	
SEQ ID NO:		1758	1758	1758	1758	1758		1759			1759					1759		,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN
1759	15d2	ក្	22	263	1.26-98	0.74	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D: T CPIT RECEPTOR	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	16d2	Щ	22	263	1.2e-98			386.70	BETA; CHAIN: E; HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1759	1dfb	Н	21	252	9.6e-94	0:30	1.00		BETA; CHAIN: B; IMMUNOGLOBULIN 3D6 FAB	
1759	1fvd	В	21	252	6.4e-96	0.41	1.00		IDED 3 IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1759	lhyx	H	21	252	4.8e-95	0.47	1.00		IMMUNOGLOBULIN 6D9; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
1759	lige	Æ	22	252	1.6e-95	0.21	1.00		COMPLEX (ANTIBODY/BINDING PROTEIN) IGGI FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1759	ligt	В	21	263	8e-99	0.42	0.99		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C

Coumpound PDB annotation	REGION, IMMUNOGLOBULIN	NIG9 (IGG1=LAMBDA=); IMMUNOGLOBULIN CHAIN: L, H; IMMUNOGLOBULIN,		ASE PEPTIDE;	F, Q; FRAGMENI, CKOSS-KEACIIVII Y, HIVI PROTEASE, ENZYME 2	INHIBITION, COMPLEX	(IMMUNOGLOBULIN/PEPTIDE)	BLOOD COAGULATION BLOOD COAGULATION, SERINE			CHIOROMETHYLKETONE   GLA, EGF, 3 COMPLEX (SEKINE CHIOROMETHYLKETONE   PROTEASE/COFACTOR/LIGAND)		NIN ISOLECTIN VI;	: A HOMOLOGOUS HEVEIN-LIKE DOMAINS	AGGLITTININ ISOLECTIN SUGAR BINDING PROTEIN LIDA-	TIN V:				/\ \\ \\ \\ \						
FOL		N1G9 (IGG1= CHAIN: L, H;	MONOCL F11.2.32; (	HIV-1 PR(	CHAIN: F, C;				FACTOR	SOLUBLE	CHIORO	(DFFRCM	AGGLUTI	CHAIN: A	AGGLUTI	VI/AGGLU	CHAIN: A;	AGGI IIT	1101000	I/AGGLU	I/AGGLUT CHAIN: A;					
SEQFOL D score								50.68									,					75 69	62.34	62.34	62.34	62.34
PMF		1.00	1.00										0.01		-0.12			0.00							0.36	0.36
Verify score		0.35	0.39										0.40	<b></b>	0.06			-0.20							-0.34	-0.34
Psi Blast		1.6e-93	3.2e-93					6e-10					1.1e-07		3e-08			6e-09	_			36.17	3e-12	3e-12	3e-12 3e-12	3e-12 3e-12
END		249	251					195					88		88			88				192	192	192	192	192
STAR T AA		21	22					64					12		12			12				37	37	37	37	37
CHAI N ID		Н	#					T					٧		Ą			∀	_				A	Ą	A	A A
PDB ID		Ingp	2hrp					Idan					1ehd		leis			len2				1ext	lext	lext	lext	lext lext
SEQ ID NO:		1759	1759					1762					1762		1762			1762				1762	1762	1762	1762	1762

				_		_		T													_							_			
PDB annotation		GP IIB/IIIA ANTAGONIST 1FVL 9	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I	RECEPTOR, STNFRI; INCF 8	BINDING PROTEIN, CYTOKINE INCF 19	SIGNALLING PROTEIN TYPE I	RECEPTOR, STNFR1; 1NCF 8	BINDING PROTEIN, CYTOKINE INCF 19	COMPLEX (BLOOD COAGULATION/INHIBITOR)	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	SIKUCIUKE, FACIOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR; ANTISTASIN CRYSTAL
Coumpound		NULL IFVL 5	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A,	B; 1NCF 5	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A,	B; INCF 5	FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: I:							ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;	
SEQFOL	D score			66.44				55.28			57.36	-												65,03							
PMF	score		-0.12		0.23													0.15												0.12	
Verify	score		0.17		-0.24													0.05												-0.14	
Psi Blast			4.5e-19	1.3e-20	7.5e-09			7.5e-11			3e-14							3e-17					,	1.5e-18						3e-18	_
END	AA		184	203	140			189			176							121					,	161						161	
STAR	TAA		15	48	17			55			41							19					ļ	23						58	
CHAI	NID				Ą			A			ı																				
PDB	<b>e</b>		1klo	1klo	Incf			lncf			1pfx							lskz						ISKZ			_			lskz	
SEQ	ΑÖ		1762	1762	1762			1762			1762							1762					į	79/1					,	1762	

PDB annotation	STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS		TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL		-	SIGNAL TRANSDUCTION PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
Coumpound		ANTISTASIN; CHAIN: NULL;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BETA-SPECTRIN; 1BTN 4 CHAIN: NULL: 1BTN 5	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;
SEQFOL D score				61.72		97.20			
PMF score		-0.08	-0.15		0.13		0.70	0.24	0.01
Verify score		0.13	0.36		0.12		-0.02	0.52	0.04
Psi Blast		4.5e-17	9e-33	0.0014	1.5e-18	6e-29	0.003	0.0043	1.2e-11
END		204	190	191	133	191	234	347	349
STAR T AA		86	35	06	13	32	200	245	245
CHAI N ID		-	A	A	A	А		А	А
PDB ID		Iskz	Ivmo	2psp	9wga	9wga	1btn	lbyn	1byn
SEQ ID NO:		1762	1762	1762	1762	1762	1768	1768	1768

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PDB annotation	ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETP A KINDHONGENATE 3 SIGNAL	TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN DAPP1, PHISH, RAM32: PI ECK STRIN 3.	PHOSPHOINOSITIDES, INOSITOL	TETRAKISPHOSPHATE 2 SIGNAL	TRANSDUCTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN NFI-333;	NEUROFIBROMIN, TYPE I	NEUROFIBROMATOSIS, NFT, RAS,	GANGED CROWTH BECLII ATTON	CAINCEN, GROW IT RECOLATION,	MUTATION, ARGININE FINGER	SIGNALING PROTEIN NF1-333;	NEUROFIBROMIN, TYPE I	NEUROFIBROMATOSIS, NF1, RAS,	GAP, 2 SIGNAL TRANSDUCTION,	CANCER, GROWTH REGULATION,	GIF 3 HIDROLISIS, FAITENI MITATION ARGININE FINGER				
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3-	CHAIN: A;			NEUROFIBROMIN; CHAIN: A;						NEUROFIBROMIN; CHAIN: A;						PHOSPHORYLATION	PLECKSTRIN (N-TERMINAL	PLECKSTRIN HOMOLOGY	DOMAIN MILLANT PINS
SEQFOL D score									108.36															
PMF score		0.54	0.36		0.70										66.0						0.37			
Verify score		0.47	0.07		-0.29									-	0.21						0.33			
Psi Blast		4.5e-05	6e-05		9e-06				7.5e-68						7.5e-68						4.5e-05			
END AA		362	235		239				289						. 289						239			
STAR T AA		247	173		173			-	400						416					_	173			
CHAI N ID		А	A		A				V					_	A									
PDB ID		1dqv	Ifao		1fb8				Infi						1nf1						1pls			_
SEQ ID NO:		1768	1768		1768				1768						1768						1768			_

ion		ON SON OF RIN, SON OF	ON IRS-1; GNAL	MAIN; VIN, CALB				GAP-334, ITVATION, INSDUCTION, ON, CANCER	GAP-334, ITVATION, INSDUCTION, IN, CANCER	N/RNA TRA MAIN, RNA
PDB annotation		SIGNAL TRANSDUCTION SON OF SEVENLESS; PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN		:		GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA
Coumpound	WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHIHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	SOS I; CHAIN: NULL;	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNA PTOTA GMIN I (FIRST C)	DOMAIN) (CALB) 1RSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	P120GAP; CHAIN: NULL;	P120GAP; CHAIN: NULL;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*
SEQFOL D score									183.05	
PMF score		0.39	0.16	0.22	0.05		0.49	1.00		-0.19
Verify score		-0.48	0.17	0.22	-0.14		0.13	0.62		0.05
Psi Blast		0.00015	3e-05	90-99	0.0043		1.5e-09	1.5e-91	1.5e-91	3.2e-14
END AA		235	245	349	347		349	712	718	205
STAR T AA		162	184	247	245		246	397	397	126
CHAI N ID			A							A
PDB ID		1pms	Iqqg	1rlw	lrsy		lrsy	l wer	Iwer	1b7f
SEQ ID NO:		1768	1768	1768	1768		1768	1768	1768	1770

	_					_				_	_		_					_													_		
PDB annotation	COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PKE-MKNA; SPLICING   REGULATION, RNP DOMAIN, RNA	COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	RNA-BINDING PROTEIN/RNA TRA	MANAGED TO THE COLUMN TWO	PKE-MKNA; SPLICING	KEGULATION, KINF DOMAIN, KINA   COMPLEX	GENE REGITI ATTON/RNA POI V/A)	BINDING DECTEIN 1 DABS 1: DDM	PROTEIN-RNA COMPI EX GENE	PEGIII ATTOMBAA	W. C. C. C. C. C. C. C. C. C. C. C. C. C.		CENTE DE CITE A TEICNICA I PORTUE	GENE KEGULA HON/KNA POLY(A)	BINDING PROTEIN I, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE
Coumpound	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; KNA (5'- R(P*GP*UP*UP*GP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(p*Gp*Up*Up*Gp*Up*Up*Up* ID*ID*ID*ID*ID*II	SXI-I FTHAI PROTFIN: CHAIN:	A P. Park (2)	A, B; KNA (5'-	INFIDATION TO THAT INFORMATION OF THE	POLYDENY! ATE RINDING	PROTEIN 1. CHAIN: A B C D	F F G H. RNA (5'L	D/* A D* A D* A D* A D* A D* A D*	AD*AD*AD*A) 29. CHAIN: M N	OPORST.	DOI VERMINI ATTENDATE	POLYDENYLAIE BINDING	FROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	0, P, Q, R, S, I;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-
SEQFOL D score																			3	>													
PMF score		-0.02			1.00			0.51	10:0			-0.01	•					70 0	0.80					,	-0.11		,				0.89		
Verify score		0.24			0.63			0.63	3			60 0						04.0	0.40					- 0	0.07						0,45		
Psi Blast		1.6e-37			4.8e-34			4 8e-14	1	-		1 6e-39	\ \ \ \ \					6 10 21	0.46-34						1.6e-32						6.4e-28		
END AA	!	314			425			431	1			320	)					/31	164					000	300						409		
STAR T AA		132			236			348	2			136	)					230	720						136						238		
CHAI N ID		Ą			A			4	4			A		_				<	- ⊄			-		T	20						В		
PDB ID		1b7f			1b7f			1b7f				1cvi	,					1000	[SS]						lcvj						lcvj		
SEQ ID NO:		1770			1770			1770	?			1770						1770	0//1						0//1						1770		

	PDB CHAI		STAR F	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	REGULATION/RNA
lcvj	<u>m</u>	352		435	1.6e-12	0.33	0.76		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, O, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
lcvj	ഥ	238		402	6.4e-21	0.17	0.65		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
lcvj	н	238		405	1.6e-21	0,03	0.25		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
lcvj	E	352			1.6e-12	0.78	0.68		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
148z	A	233			3.2e-21	0.04	0.19		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1d8z	4	346		431	4.8e-13	0.52	0.27		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1d9a	∢	136			8e-14	0.03	-0.19		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1d9a	<b>∀</b>	237		319	3.2e-18	0.48	-0.03		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-

F		Т		_		Τ.				Т																		-		
PDB annotation	BINDING DOMAIN	RIBONUCLEOPROTEIN U1A117; RIBONUCLEOPROTEIN. RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR RIBONITCLEOPROTEIN A 1	NUCLEAR PROTEIN, HNRNP, RBD.	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	KIBONUCLEOPKOLEIN AI,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	
Coumpound	A00000 AND -1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A:	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;		HNRNP A1; CHAIN: NULL;					HNRNP A1; CHAIN: NULL;		•				HNRNP A1; CHAIN: NULL;						HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN D0;	CHAIN: A;	HETEROGENEOUS NUCLEAR	KIBONUCLEOPROTEIN DO;	HETEROGENEOUS NITCLEAR	RIBONUCLEOPROTEIN DO:	CHAIN: A;
SEQFOL D score																														
PMF		0.12		0.07		-0.09					0.95						0.94						-0.19			0.16		0.68		
Verify score		0.57		0.30		0.17					0.21						0.83						0.03			0.78		0.91	·	
Psi Blast		1.6e-11		3.2e-12		4.8e-45					1.6e-40						1.3e-16						6.4e-20			4.8e-22		9.6e-15		
END AA		315		313		314	·				425						431						213			314		425	<u> </u>	
STAR T AA		230		222		129					231						350						136			237		351		
CHAI N ID				∀																	,		∀			Ą		V	-	
PDB ID		1fht		1fjc		1ha1				,	lhal						lha1						1hd1			1hd1		IhdI		
SEQ ID NO:		1770		1770		1770				i	17/0						1770						1770			1770		1770		

PDB annotation	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING,
Coumpound	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD
SEQFOL D score									
PMF score	0.15	-0.15	0.13	-0.18	0.17	66.0	0.25	0.70	0.88
Verify score	0.06	0.21	0.51	0.11	0.74	0.91	0.36	0.42	0.75
Psi Blast	4.8e-19	1.6e-18	3.2e-13	1.3e-14	6.4e-19	4.8e-14	1.1e-19	4.8e-14	6.4e-18
END AA	427	319	429	213	314	425	322	431	314
STAR T AA	238	223	341	136	237	351	236	348	236
CHAI N ID	A			А	A	А			A
PDB ID	1qm9	1sxl	lsxl	2mss	2mss	2mss	2sxl	2sxl	2u2f
SEQ NO.	1770	1770	1770	1770	1770	1770	1770	1770	1770

PDB annotation	U2 SNRNP, RBD, RNA-BINDING	PROTEIN	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HINKINF AI, UPI; COMPLEX	(RIBONUCLEOPROTEIN/DNA),	HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX	(RIBONUCLEOPROTEIN/DNA)	HNRNP A1, UP1; COMPLEX	(RIBONUCLEOPROTEIN/DNA),	HETEROGENEOUS NUCLEAR 2	RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INFIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA	BINDING DOMAIN, RBD, RNA	RECOGNITION MOTIF, RRM, 2	SPLICING INHIBITOR,	TRANSLATIONAL INHIBITOR, SEX 3	DETERMINATION, X CHROMOSOME	DOSAGE COMPENSATION	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROJEIN	COMPLEX (ZINC FINGER/DNA) ZINC
Coumpound	SUBUNIT; CHAIN: A;		HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1;	CHAIN: A; 12-NUCLEUIIDE	SINGLE-STRANDED	1ELUMETRIC DNA; CHAIN; B;	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1;	CHAIN: A; 12-NUCLEOTIDE	SINGLE-STRANDED	TELOMETRIC DNA; CHAIN: B;		SEX-LETHAL; CHAIN: A, B, C;							SEX-LETHAL; CHAIN: A, B, C;							QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SILE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;
SEQFOL	31036																											74.27				
PMF	31036		60.0					0.52						-0.02							96.0											0.04
Verify	3636		0.00					09.0						0.22							0.32										,	-0.22
Psi Blast	-		4.8e-47					1.6e-43						3.2e-36							1.4e-32							3.2e-31		•	:	9.6e-44
END			319					433						307							425							445				219
STAR			128					231						133							236							363				138
CHAI	9		A					Ą						∢							A							¥				[د
PDB			2up1					2up1						3sxl	_						3sxl							la1h				Imey
SEQ	NO.		1770					1770						1770							1770							1772				7//1

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PDB annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		TEITIA: CHAIN: A D: 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;
SEQFOL D score																															100.49
PMF score		0.05				0.29				0.54							96.0							0.99							
Verify score		0.55				-0.73				0.24							0.28							0.07							
Psi Blast		9.6e-11				1.6e-09				1.3e-35							4.8e-37			•			,	3.2e-38							3.2e-38
END		191				71				312	)						368							452							497
STAR T AA		164				44			_	167	; 	_		_			223						- 0	307							334
CHAI N ID		<sub>O</sub>				ڻ ڻ				A	l						A						-	∀	-						A
PDB ID		lmey				Imey				11f6							1tt@						2	1t16 							1tf6
SEQ ID NO:		1772				1772				1772							1772						1	17772							1772

PDB annotation	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION
Coumpound	CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF score		0.95	0.94	0.11	0.72
Verify score		-0.06	0.01	0.07	-0.21
Psi Blast		1.6e-37	1.4e-36	4.8e-32	1.5e-23
END		509	529	247	275
STAR T AA		363	391	143	169
CHAI N ID		Ą	А	၁	ŭ
PDB ID		14f6	14f6	1ubd	lubd
SEQ ID NO:		1772	1772	1772	1772

										-						
REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION.	INITIATOR ELEMENT, YY1, ZINC 2	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	INTIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGIN ATIONONA)	COMPLEX (TRANSCRIPTION
	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;		YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA:	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR FI FMENT DNA:	CHAIN: A, B;				YY1; CHAIN: C; ADENO-
	1.00		1.00		1.00				_	1.00						1.00
	0.13		0.02		0.21					0.36						0.03
	4.5e-43		1.6e-32		1.5e-46	v				4.8e-34						1.5e-50
	303		303		359					359						443
	199		202		223					258						332
	C		ပ		C					၁						S
	pqn1		lubd		1ubd		•			lubd						1ubd
	1772		1772		1772					1772						1772
		C 199 303 4.5e-43 0.13 1.00 YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	1ubd         C         199         303         4.5e-43         0.13         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           Intitator Element DNA; CHAIN: A, B;	1ubd         C         199         303         4.5e-43         0.13         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           Iubd         C         202         303         1.6e-32         0.02         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           Iubd         C         202         303         1.6e-32         0.02         1.00         XY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           Iubd         C         202         303         1.6e-32         0.02         1.00         ASSOCIATED VIRUS P5           Initiator Element DNA;         CHAIN: A, B;         CHAIN: A, B;         CHAIN: A, B;	1ubd         C         202         303         4.5e-43         0.13         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           1ubd         C         202         303         1.6e-32         0.02         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           1ubd         C         202         303         1.6e-32         0.02         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           1ubd         C         ASSOCIATED VIRUS P5         INITIATOR ELEMENT DNA; CHAIN: A, B;	1ubd         C         202         303         4.5e-43         0.13         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           1ubd         C         202         303         1.6e-32         0.02         1.00         YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5           1ubd         C         223         359         1.5e-46         0.21         1.00         YY1; CHAIN: C; ADENO-YY1; C	Tubd   C   199   303   4.5e-43   0.13   1.00   YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5   Interest of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con	Tubd   C   199   303   4.5e-43   0.13   1.00   YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5   Interpretation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t	Tubd   C   199   303   4.5e-43   0.13   1.00   YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5   Interest of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con	Tubd   C   199   303   4.5e-43   0.13   1.00   YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	Tubd   C   199   303   4.5e-43   0.13   1.00   YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5	Tubd   C   199   303   4.56-43   0.13   1.00   ASSOCIATED VIRUS PS	Tubd   C   199   303   4.5e-43   0.13   1.00   ASSOCIATED VIRUS P5	Tubd   C   199   303   4.5c-43   0.13   1.00   ASSOCIATED VIRUS P5	Tubd   C   199   303   4.5e-43   0.13   1.00   ASSOCIATED VIRUS P5	Tubd   C   199   303   4.5c-43   0.13   1.00   ASSOCIATED VIRUS P5

PDB annotation		REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN. DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION.	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN  PECOGNITION 3 COMPLEY	TECOGNITION, S COME LESS (TE ANICO ID TION)	(FINAL TION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	INTIATOR ELEMENT YVI. ZINC.2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	COMPLEY (TP ANSCRIPTION	REGITTATION/DNA) YING-YANG 1	TRANSCRIPTION INITIATION.	INITIATOR ELEMENT, YYI, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,
Coumpound		ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	CHAIN: A. B.				VV1. CHAIN: C. ADENO	ASSOCIATED VIRIS P5	INITIATOR ELEMENT DNA:	CHAIN: A, B;			,		YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;
SEQFOL	D score																		_					_		82.44		
PMF	score					1.00						0.60						1 00	2									
Verify	score					90.0						-0.01						0.01	•									
Psi Blast						6e-52						9e-51						36-50	) )					_		9e-51		
END						472						499						527	i							528		
STAR	TAA					360						388						416	2							420		
CHAI	9 Z			_		သ		_				ပ					_	0	)			_				ပ		
PDB	<u>e</u>					1ubd						lubd						111hd								lubd		
SEQ	e ë					1772						1772						1777	!				_			1772		

PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ADR1; CHAIN: NULL;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII;
SEQFOL D score								
PMF		1.00	-0.18	0.13	0.95	1.00	66.0	0.98
Verify		0.11	0.11	-0.10	0.26	0.51	0.21	0.31
Psi Blast		8e-35	8e-14	3.2e-29	3e-58	9e-64	1.5e-63	1.5e-67
END AA		527	193	246	389	417	445	501
STAR T AA		426	139	102	197	278	306	362
CHAI N ID		ပ		A	A	A	Ą	A
PDB ID		lubd	2adr	2gli	2gli	2gli	2gli	2gli
SEQ ID NO:		1772	1772	1772	1772	1772	1772	1772

PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION			LIGASE CBL, UBCH7, ZAP-70, E2, UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	LIGASE CBL, UBCH7, ZAP-70, E2,
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL; CHAIN: A; ZAP. 70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C.	SIGNAL TRANSDUCTION
SEQFOL D score		88.77		,					
PMF score			0.84	1.00	0.07	0.52	0.39	0.41	0.21
Verify score			-0.07	0.24	-0.87	-0.50	-0.28	0.41	-0.34
Psi Blast		1.5e-67	1.5e-49	1.6e-34	4.8e-06	1.3e-11	3.2e-06	1.2e-12	3.2e-06
END		501	524	529	59	59	, .	69	59
STAR T AA		362	390	398	10	11	51	14	15
CHAI N ID		A	Ą	A				Ą	A
PDB ID		2gli	2gli	2gli	1bor	1chc	[chc	1fbv	1fbv
SEQ ID NO:		1772	1772	1772	1774	1774	1774	1774	1774

PDB annotation	P- UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING FINGER PROTEIN MAT1; RING FINGER (C3HC4)		DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANIDEM 2 THE IT YOU EN COIL S
Coumpound	PROTEIN CBL; CHAIN: A; ZAP-70 PEPTIDE; CHAIN: B; UBIQUITIN-CONJUGATING ENZYME E12-18 KDA UBCH7; CHAIN: C;	NUCLEAR FACTOR XNF7; CHAIN: NULL;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RAG1; CHAIN: NULL;	RAG1; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				54.69			
PMF score		0.36	0.74		0.84	0.01	0.19
Verify score		-0.23	0.21		-0.03	-0.19	-0.07
Psi Blast		1.5e-13	4.5e-14	3e-06	4.5e- <u>2</u> 0	6.4e-14	4.5e-07
END		128	70	304	100	109	414
STAR T AA		93	111	63	11	6	248
CHAI N ID		t	A	A			A
PDB ID		lfre	1g25	1quu	lrmd	1rmd	1cun
SEQ F)		1774	1774	1774	1774	1774	1775

PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE		TRANSCRIPTION HELIX-BUNDLE	TRANSCRIPTION TRANSCRIPTION, RNA POLYMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, EXTREMOPHILE		
Coumpound		ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	TRANSCRIPTION ELONGATION FACTOR S-II; CHAIN: A;	RNA POLYMERASE II; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII (TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII
SEQFOL D score								2
PMF		-0.13	-0.12	0.18	0.52	0.51	00.1	0.75
Verify score		0.34	0.10	0.21	-0.14	-0.51	0.16	-0.07
Psi Blast		9e-10	4.5e-09	0.0006	4.5e-06	0.00045	1.6e-10	4.5e-11
END AA		93	124	553	78	343	345	343
STAR T AA			6	516	-	291	286	287
CHAI N ID		¥	A		А			
PDB ID		lcun	lez3	1chc	1eo0	lqyp	1tfi	1tfi
SEQ ID NO:		1776	1776	1777	1780	1780	1780	1780

PDB annotation	DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE- PROTEIN KINASE, PHOSPHORYLATION, 3 ALDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXXP MOTIF	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN		COMPLEX (KINASE/PEPTIDE)
Coumpound	PROTEIN; CHAIN; B, D;	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	GRB2; CHAIN: A; SOS-1; CHAIN: B;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA;
SEQFOL D score					
PMF score		1.00	0.84	0.74	0.01
Verify score	:	0.07	-0.33	-0.35	-0.41
Psi Blast		le-11	1.4e-12	3e-13	4.8e-19
END AA		508	508	510	581
STAR T AA		457	454	446	456
CHAI N ID		A	A	A	A
PDB ID		lfyn	1gbq	1gbr	11ck
SEQ ID NO:		1781	1781	1781	1781

PDB annotation			COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3	DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX	(TRANSFERASE/PEPTIDE)	CIRCULAR PERMUTANT PWT;	CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON	TYROSINE KINASE TYROSINE	KINASE-INHIBITOR COMPLEX,	DOWN-REGULATED KINASE, 2	OKDERED ACTIVATION LOOP	CYTOSKELETON CYTOSKELETON, MEMBRANF SH3 DOMAIN	TYROSINE-PROTEIN KINASE	BRUTONS TYROSINE KINASE, B	CELL PROGENITOR KINASE,	TRANSFERASE, TYROSINE-	PROTEIN KINASE,	PHOSPHORYLATION, 2 SH3 DOMAIN	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s				CELL CYCLE/GENE REGULATION	COMPLEX, SIGNAL	TRANSDUCTION,	PHOSPHOTYROSINE BINDING 2	DOMAIN (PTB), ASYMETR IC CELL	REGULATION	TRANSFERASE HCK; SH3, PROTEIN
Coumpound		1LCK 14 CHAIN: B; 1LCK 15	C-SRC; CHAIN; C; NLJ (MN7- MN2-MN1-PLPPLP); CHAIN: N;			ALPHA SPECTRIN; CHAIN:	NULL;	HAEMATOPOETIC CELL	KINASE (HCK); CHAIN: A;			ALPHA II SPECTRIN; CHAIN: A;	TYROSINE-PROTEIN KINASE	BTK; CHAIN: A;					PHOSPHOTRANSFERASE FYN	PROTO-ONCOGENE TYROSINE	KINASE (E.C.2.7.1.112) 1SHF 3	(SH3 DOMAIN) ISHF 4	NUMB PROTEIN; CHAIN: A;	GPPY PEPTIDE; CHAIN: B;					HEMATOPOIETIC CELL
SEQFOL D score	D score																									_	•		
PMF	3000		1.00			1.00		0.15			,	00.1	0.81						1.00				0.64						1.00
Verify	3000		0.18			0.21		-0.31				0.20	-0.05						-0.64				0.25						0.46
Psi Blast			3e-11			3e-10		3.2e-18			,	1.5e-10	3e-12						7.5e-11				3e-12						7.5e-12
END	A.A.		507			208		581				208	508						508				153						508
STAR			459			457		456				457	455				•		459 .				27						455
CHAI			ت ت					A				∢	A						Ą				A	_			_		
PDB	1		1nlo			1pwt		Iqef			+	Iqkw	Iqly		_		_		1shf			-+	2nmb						4hck
SEQ	NO:		1781			1781		1781			,	1/81	1781						1781				1781						1781

PDBCHAISTARENDPsi BlastVerifyIDN IDT AAAAscore	STAR END Psi Blast T AA AA	END Psi Blast AA	Psi Blast		Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
								KINASE; CHAIN: NULL;	TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1bg1 A 36 198 1.1e-07 0.07	36 198 1.1e-07 0.07	198 1.1e-07 0.07	1.1e-07 0.07	27 0.07		 0.04		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION
1bz4 A 9 126 1.6e-05 0.20	9 126 1.6e-05	126 1.6e-05	1.6e-05	)5	0.20	0.04		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3; LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
lcun A 24 259 3e-13 0.04	24 259 3e-13	259 3e-13	36-13	,	0.04	-0.06		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1dn1 B 78 298 7.5e-19 -0.22	78 298 7.5e-19	298 7.5e-19	7.5e-19	6	-0.22	0.30		SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1ez3 A 118 260 4.5e-07 0.11	118 260 4.5e-07	260 4.5e-07	4.5e-07	7(	0.11	0.28		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
lez3 A 138 298 1.5e-08 -0.41	138 298 1.5e-08	298 1.5e-08	1.5e-08	8(	-0.41	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
lez3 A 246 394 le-09 -0.04	246 394 1e-09	394 1e-09	1e-09		-0.04	0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE

	r	T		<del></del>				
PDB annotation	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	DNA-BINDING HMGA DNA- BINDING HMG-BOX DOMAIN A OF RAT HMG1; 1AAB 8 HMG-BOX 1AAB 20	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPPNP, GPPNHP.	SERINE/THREONINE PROTEIN-KINASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, 2 PROTO-ONCOGENE, ZINC, ATP-BINDING, PHORBOL-ESTER BINDING		SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8
Coumpound	SSO1 PROTEIN; CHAIN: A;	SSO1 PROTEIN; CHAIN: A;	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	NTERFERON-INDUCED GUANYLATE-BINDING PROTEIN I; CHAIN: A;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN I; CHAIN: A;	RAF-1; CHAIN: NULL;	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA- BINDING 1HME 3 HMG-BOX DOMAIN B OF RAT HMG1) (NMR, 1 STRUCTURE) 1HME 4	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,
SEQFOL D score								
PMF score	0.04	0.03	0.03	0.19	0.04	0.03	0.00	0.12
Verify score	-0.09	-0.28	-0.24	0.02	0.02	-0.40	-0.29	0.02
Psi Blast	7.5e-07	le-11	0.00012	4.5e-05	0.00015	0.003	0.0045	0.006
END AA	485	280	763	2333	2333	66	753	141
STAR T AA	283	59	716	2237	2237	69	716	17
CHAI N ID	А	А		Ą	Æ			A
PDB ID	1fio	1fio	1aab	14g3	1f5n	Ifaq	Ihme	lncf
SEQ ID NO:	1782	1782	1783	1783	1783	1783	1783	1783

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PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	PHOSPHOTRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	GENE REGULATION/DNA LEF-1 HMG; LEF1, HMG, TCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
Coumpound	B; 1NCF 5	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN; B; DNA (5'- CHAIN: C;	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO
SEQFOL D score								
PMF score		0.23	0.31	0.41	0.31	0.01	0.45	-0.13
Verify score		0.02	-0.09	-0.35	-0.13	-0.65	-0.30	0.07
Psi Blast		0.003	0.00075	0.006	7.5e-05	0.0009	3.2e-26	3.2e-12
END AA		50	50	66	763	137	130	232
STAR T AA		21	21	69	716	100	62	178
CHAI N ID					A		А	
PDB ID		1ptq	1tbn	Itbn	2lef	Itbn	1a1h	1660
SEQ O	Š	1783	1783	1783	1783	1784	1785	1785

PDB annotation			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,
Coumpound	4	DNA-BINDING PROTEIN HUMAN ENHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (C11ABU) (NMR, 60 STRUCTURES) 1BBO	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ADR1; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score							
PMF score		0.04	0.04	0.04	0.05	0.90	0.52
Verify		-0.88	-0.42	-0.19	-0.23	-0.01	-0.23
Psi Blast		1.6e-12	1.6e-42	4.8e-41	3.2e-12	4.8e-18	8e-34
END		113	98	114	114	117	157
STAR T AA		64	15	43	87	62	18
CHAI N ID	-		ပ	ပ	Ð		В
PDB ID		1660	Imey	Imey	Imey	2adr	lawc
SEQ ID NO:	•	1785	1785	1785	1785	1785	

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PDB annotation	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA:	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6; P16INK4A,	MTSI; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	CDK, INK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;				P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; MULTIPLE	TUMOR SUPPRESSOR; CHAIN:	;;						CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	_ B;				CYCLIN-DEPENDENT KINASE
SEQFOL D score																																
PMF score		0.29	-					0.19			0.04		_							0.00				-		0.37						0.15
Verify score		-0.09						-0.01			0.14									-0.17						0.01						-0.12
Psi Blast		4.8e-29						8e-27			6.4e-17									6.4e-26						1.3e-23						6.4e-25
END AA		125						160			995									091						183						130
STAR T AA		င						21			443									.21						20						
CHAI N ID		В									В									В						Д						А
PDB ID		lawc						11648			1bi7									1blx						1blx						1bu9
SEQ ID NO:		1788						1788			1788									1788						1788						1788

PDB annotation	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	SIGNALING PROTEIN RUB1, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING PROTEIN	DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITIN, DE NOVO PROTEIN, UBIQUITIN	SIGNALING PROTEIN NEDD8; NEDD8, NEDD-8, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2 PROTEIN	
Coumpound	6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	UBIQUITIN-LIKE PROTEIN 7, RUB1; CHAIN: A;	ID8 UBIQUITIN; CHAIN: A;	UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	UBIQUITIN TETRAUBIQUITIN ITBE 3
SEQFOL D score									
PMF score		9.06	0.10	0.37	0.01	0.92	0.76	0.75	0.94
Verify		0.14	-0.12	0.01	0.14	0.17	0.02	0.22	0.48
Psi Blast		1.6e-17	1.3e-25	3.26-24	1.6e-20	1,4e-20	1.6e-27	6.4e-20	3.2e-27
END AA		267	161	129	127	194	196	195	193
STAR T AA		443	18	_	19	124	124	124	124
CHAI N ID		А	Ą	∢		A	A	Ą	В
PDB ID		1d9s	lihb	lihb	lmyo	15t0	1c3t	1ndd	1tbe
SEQ ID NO:		1788	1788	1788	1788	1791	1791	1791	1791

PDB annotation		UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL, ELONGATION	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POI YPROTEIN MYRISTYLATION	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCITM RINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TR1C- DOMAIN, RESIDIJES 1 - 75; CERIUM-
Coumpound	CHROMOSOMAL PROTEIN UBIQUITIN 1UBI 3	UBIQUITIN CORE MUTANT 1D7; CHAIN: A;	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CALMODULIN; CHAIN: NULL;
SEQFOL D score					69.49			57.92		
PMF score	99.0	0.55	0.15	0.64		0.00	0.00		0.25	-0.01
Verify	0.19	0.39	-0.54	-0.22		-0.04	-0.04		0.30	0.12
Psi Blast	4.8e-29	3.2e-28	6.4e-05	3,2e-36	3.2e-36	0.0075	0.0075	6.4e-36	6.4e-36	4.8e-16
END	196	196	181	92	92	227	235	382	379	309
STAR T AA	124	124	124	11	-	157	165	225	241	241
CHAI N ID		A	A			В	В			
PDB ID	lubi	1nd7	lvcb	1bax	1bах	1dn1	1dn1	laj4	1aj4	1ak8
SEQ ID NO:	1791	1421	1791	1792	1792	1794	1795	1799	1799	1799

2	TAA	V		SCOTE	FINIE	SEQFOL Decore	Coumpound	PDB annotation
	_			31035	2 1026	2 1025 7	:	
								LOADED, CALCIUM-BINDING PROTEIN
1	241	314	1.4e-12	0.50	-0.01		CARDIAC N-TROPONIN C;	CALCIUM-BINDING CNTNC;
							CHAIN: NULL;	CALCIUM-BINDING, REGULATION,
								TROPONIN C, CARDIAC MUSCLE 2
1	233	391	4.8e-42			69.73	SERINE/THREONINE	HYDROLASE CALCINEURIN;
							PHOSPHATASE 2B; CHAIN: A,	HYDROLASE, PHOSPHATASE,
							B;	IMMUNOSUPPRESSION
	240	378	4.8e-42	0.46	0.68		SERINE/THREONINE	HYDROLASE CALCINEURIN;
							PHOSPHATASE 2B; CHAIN: A,	HYDROLASE, PHOSPHATASE,
-							B;	IMMUNOSUPPRESSION
	202	345	3.2e-11	-0.02	0.19		NEUROCALCIN DELTA;	CALCIUM-BINDING CALCIUM-
							CHAIN: A, B;	BINDING, MYRISTOYLATION,
								NEURONAL SPECIFIC GUANYLATE
								2 CYCLASE ACTIVATOR
	224	385	6.4e-36	0.64	0.83		NEUROCALCIN DELTA;	CALCIUM-BINDING CALCIUM-
							CHAIN: A, B;	BINDING, MYRISTOYLATION,
								NEURONAL SPECIFIC GUANYLATE
								2 CYCLASE ACTIVATOR
	224	390	6.4e-36			59.92	NEUROCALCIN DELTA;	CALCIUM-BINDING CALCIUM-
							CHAIN: A, B;	BINDING, MYRISTOYLATION,
								NEURONAL SPECIFIC GUANYLATE
	241	378	3.2e-42	0.25	0.18		CALCIUM-BINDING PROTEIN	ACITATION GENERALON
							CALMODULIN COMPLEXED	
							WITH CALMODULIN-BINDING	
							DOMAIN OF 1CDM 3	
							CALMODULIN-DEPENDENT	
							PROTEIN KINASE II 1CDM 4	
	241	378	3.2e-47	0.05	0.21		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE)	
							1CLL 3	-
-	241	380	3.2e-47			59.19	CALCIUM-BINDING PROTEIN	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ö	<b>e</b>	OI N	TAA	AA		score	score	D score		
									CALMODULIN (VERTEBRATE) ICLL 3	
1799	1cmf		242	309	4.8e-11	0.73	0.13		CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9
1799	1cmf		310	378	1.6e-25	0.43	-0.06		CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9
1799	1dgv	A	241	388	3.2e-20	0.01	09:0		APO CIB; CHAIN: A	BLOOD CLOTTING HELICAL, EF- HAND, BLOOD CLOTTING
1799	1dtl	А	183	306	1.4e-12	90.0	0.07		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
1799	1dt]	A	241	379	8e-36	0.16	69:0		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX- TURN-HELIX
1799	lexr	А	241	378	1.3e-44	0.13	0.12		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1799	1471	A	247	309	8e-11	0.40	09:0		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1f71	А	316	378	3.2e-24	0.44	0.16		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1799	1fi5	Ą	238	908	9.6e-10	0.25	0.21		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1fi5	A	313	379	1.3e-19	0.10	0.18		TROPONIN C; CHAIN: A;	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN
1799	1fpw	А	221	341	3.2e-15	0.18	0.03		CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	METAL BINDING PROTEIN YEAST FREQUENIN EF-HAND, CALCIUM
1799	ljba	A	241	392	1.6e-29	0.46	0.99		GUANYLATE CYCLASE ACTIVATING PROTEIN 2;	LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN,

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ID NO:	<b>Q</b>	NID	TAA	AA		score	score	D score		
									CHAIN: A;	GUANYLYL CYCLASE 2 REGULATION
1799	Itcf		232	378	3.2e-37	0.10	0.48		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE
										CONTRACTION MUSCLE
										BINDING, TROPONIN, E-F HAND, 2
										OPEN CONFORMATION
<u>-</u>		,								REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE
										CONTRACTION
1799	1tcf		233	379	3.2e-37			63.35	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE
										CONTRACTION CALCITM-
<del></del>										BINDING, TROPONIN, E-F HÁND, 2
					•					OPEN CONFORMATION
										REGULATORY DOMAIN, CALCIUM-
										REGULATED 3 MUSCLE
1799	1tnx		233	378	4.8e-36			69.19	TROPONIN C; ITNX 4 CHAIN:	CALCIUM-BINDING PROTEIN EF.
									NULL; 1TNX 5	HAND 1TNX 14
1799	1tnx		236	378	4.8e-36	-0.22	0.05		TROPONIN C; 1TNX 4 CHAIN:	CALCIUM-BINDING PROTEIN EF-
1									NULL; 1TNX 5	HAND 1TNX 14
1799	Itop	!	227	382	3.2e-38			64.51	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1799	1top		236	378	3.2e-38	0.02	0.41		CONTRACTILE SYSTEM	
									PROTEIN TROPONIN C 1TOP 3	
1799	1trc	Ą	242	306	6.4e-11	0.28	-0.05		CALCIUM BINDING PROTEIN	
				,,					CALMODULIN (/TR=2=C\$	
-									PRAGIMENT COMPRISING	
									THE INTACT MOT BOTH EVITED	
									THE INTACT MOLECOLE) TIRC	
1799	1trc	٧	314	378	1.1e-24	0.03	-0.09		CALCIUM BINDING PROTEIN	
									CALMODULIN (/1K=2=C\$	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ö	a —	<u> </u>	TAA	AA		score	score	D score		
									FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1799	1vrk	A	180	309	1.6e-14	-0.21	0.07		CALMODULÍN; CHAIN: A; RS20; CHAIN: B;	CALMODULM, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	lvrk	Ą	239	381	3.2e-46			56.76	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	lvrk	Ą	241	378	3.2e-46	0.12	0.33		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1799	1wdc	၁	241	382	1.4e-20	0.23	0.04		SCALLOP MYOSIN; CHAIN: A, B, C;	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN
1799	3ctn		238	306	9.6e-10	0.36	0.13		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1799	3ctn		313	379	1.3e-19	0.19	0.12		TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN
1801	1a1h	A	120	210	1.6e-12	0.03	0.35		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1801	la1h	Ą	158	238	4.8e-19	0.03	0.98		QGSR ZINC FINGER PEPTIDE; 'CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

	<del>,</del>	·	T						
PDB annotation	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA),
Coumpound	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score	84,50								
PMF		1.00	0.41	0.57	0.66	0.78	0.15	1.00	1.00
Verify score		0.23	-0.16	0.22	0.11	0.07	0.17	0.45	0.54
Psi Blast	4.5e-37	1.1e-29	9.6e-22	1.6e-19	3e-19	3e-21	3.2e-26	8e-30	9e-31
END	296	377	377	404	454	481	481	509	510
STAR T AA	214	270	270	298	298	353	382	429	429
CHAI N ID	A	Ą	Ą	Ą	Ą	Ą	Ą	A	А
PDB ID	lalh	lalh	laIh	lalh	lalh	laIh	1aIh	lalh	1alh
SEQ ID NO:	1801	1801	1801	1801	1801	1801	1801	1801	1801

PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA).	ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA NTER ACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A: DUPLEX	OLIGONUCLEOTIDE BINDING	OGSR ZINC FINGER PEPTIDE:	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER PROTFIN: CHAIN: C F G:			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	
SEQFOL D score																												•	
PMF score		1.00		1.00	)		0.36				1.00					1.00					1.00					1.00			
Verify score		-0.09		0.28	}		0.10				0.42					0.55					0.35					0.56			
Psi Blast		1.1e-30		7.5e-34			8e-30				1.4e-37					3.2c-47					3.2e-48					4.8e-49			
END AA		537		565	} }		210				238					566					294					322			
STAR T AA		457		485	}		119				157					185					213					241			
CHAI N ID		A		A			S				C					ပ					၁					ں د			
PDB ID		lalh		la1h			1mey				1mey		-			1mey					lmey					1mey			
SEQ ID		1801		1801	}		1801				1801			-		1801					1801					1801			

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
NO.	<u>a</u>	NB	TAA	AA		score	score	D score		,
										(ZINC FINGER/DNA)
1801	lmey	2	241	323	4.8e-49			101.14	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
					-					CRYSTAL STRUCTURE, COMPLEX
, ,	,	Ĭ		ļ			ļ			(ZINC FINGER/DNA)
1801	Imey	ပ	569	377	4.8e-40	-0.06	0.51		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	lmey	ပ	297	453	1.1e-20	0.01	-0.17		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
_									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
									,	(ZINC FINGER/DNA)
1801	1mey	ပ	353	481	1.3e-22	0.42	0.70		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
								-	CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	lmey	ပ	357	453	8e-41	0.41	0.24		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
			_						PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
			•							CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	lmey	ပ	381	481	3.2e-45	0.26	0.07		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									,	CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	Imey	ပ	428	509	1.6e-49	0.51	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2

PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	Chyceral offeriory mer Colorery	CRISIAL SINOCIONE, COMPLEA (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 58 RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
Coumpound		DNA; CHAIN: A, B, D, E;	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROIEIN; CHAIN: C, F, G;		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;			
SEQFOL D score																									114.65					
PMF		66'0				1.00				-0.01								0.22												
Verify score		-0.03				0.25				0.23								0.08												
Psi Blast		1.6e-49				1.6e-49			•	6.4e-17					=			1.4e-22							3e-61					
END		537			ļ	565				481								247							325					
STAR T AA		456				484				382								112							157					
CHAI N ID		၁				<u></u>				Ą								٧							A					
PDB ID		lmey				lmey				14f3								1tf6							1tte					
SEQ ID NO:		1801			,	1801				1801								1801							1801					

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PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER, PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC
Coumpound	TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN': A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
SEQFOL D score					
PMF score	0.99	1.00	0.24	0.28	0.99
Verify score	0.37	0.15	0.04	-0.15	0.23
Psi Blast	9.6e-31	1.4e-35	1.3e-25	1.3e-34	1.6e-35
END	303	324	495	547	565
STAR T AA	158	186	298	382	429
CHAI N ID	Ą	<b>∀</b>	Ą	Ą	A
PDB ID	1tf6	1tf6	1tf6	14f6	1tf6
SEQ ID NO:	1801	1801	1801	1801	1801

PDB annotation	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONIDNA) YING-YANG 1:		INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	KECOGNITION, 3 COMPLEX	(TRANSCRIPTION   REGULATION/DNA)	COMPLEX (TRANSCRIPTION			FINGER PROTEIN DNA PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION			INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION			INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	KEGULAIION/DNA)
Coumpound		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CITAIN: A, B,				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				
SEQFOL D score								92.90																						
PMF score		1.00													1.00								1.00							
Verify score		0.25													0.35								0.15							
Psi Blast		6e-43						7.5e-48							7.5e-48								7.5e-51		_					
END		266						267							294								322							
STAR T AA		157						159							186								217							
CHAI N ID		၁		-				C					·		၁								ر ن		_					
PDB ID		lubd						Iubd							Iubd							,	1ubd							
SEQ UD NO:		1801	_					1801							1801							,	1801							

PDB annotation	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
SEQFOL D score					
PMF score		0.99	-0.02	0.64	0.36
Verify score		-0.16	0.04	0.23	0.26
Psi Blast		3.2e-26	1.6e-24	1.5e-30	6.4e-29
END		377	453	509	481
STAR T AA		249	305	351	360
CHAI N ID		O	v	ن ن	ပ
PDB ID		lubd	Iubd	1ubd	lubd
SEQ NO.		1801	1801	1801	1801

PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	
PDB	INITIATOR ELEMENT, YY1, FINGER PROTEIN, DNA-PRC RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YA TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, Z FINGER PROTEIN, DNA-PROT RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YA TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, Z FINGER PROTEIN, DNA-PROT RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YA TRANSCRIPTION INITIATION INITIATOR ELEMENT, YY1, Z FINGER PROTEIN, DNA-PROT RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3
SEQFOL D score					
PMF score		0.65	1.00	0.98	0.10
Verify	A	0.07	0.30	-0.10	0.53
Psi Blast		3.26-31	4.5e-40	8e-34	3e-18
END		509	565	565	377
STAR T AA		387	454	464	294
CHAI N ID		ပ	၁	၁	Y
PDB ID		1ubd	lubd	lubd	2drp
SEQ ID	NO:	1801	1801	1801	1801

PDB annotation		JI; COMPLEX (DNA-BINDING , D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	JI; COMPLEX (DNA-BINDING , D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)					JI; COMPLEX (DNA-BINDING , D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)		-
Coumpound	DNA 2DRP 4	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	
SEQFOL D score		100.58			`					
PMF score			1.00	0.90	0.81	0.49	-0.02	0.87	0.75	,
Verify score			0.25	0.15	0.01	0.11	0.15	0.40	0.25	000
Psi Blast		1.1e-58	3e-57	1.1e-58	3.2e-23	1.1e-37	8e-30	6.4e-32	1.5e-48	, ,
END		296	296	322	404	511	508	536	565	100
STAR T AA		157	157	185	249	297	360	424	428	707
CHAI N ID		Ą	A	A	A	A	A	Ą	Ą	*
PDB ID		2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli	:
SEQ ID NO:		1801	1801	1801	1801	1801	1801	1801	1801	1001

score D score
59.81
0.83
74.73
0.98
67.59
0.18
1.00
0.48
0.65

REGEPTOR, LEUCOCVTE, CTYPE		CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
250 1e-24 63.07 MANNOSE-BINDING PROTEIN; COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: CLASS IH-2DD HEAVY CHAIN: CHAIN: A, BETA-2- MICROGLOBULIN; CHAIN: B, HIV ENVELOPE GLYCOPROTEIN: C, D; CHAIN: P, LY49A; CHAIN: C, D; CHAIN: P, LY49A; CHAIN: C, D;										RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR
250 16-24 65.37 COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, B, F; COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: CHAIN: CHAIN: A; C52 36-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; C53 1.56-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; A; BETA-2-MICROGLOBULIN; CHAIN: B; HIY ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D; CHAIN: P; LY49A; CHAIN: C, D; CHAIN: P; LY49A; CHAIN: C, D; CHAIN: P; LY49A; CHAIN: C, D;	<u> </u>		86	249	36-27			63.07	MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN: NULL; 1HUP 5	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL 1HUP 12
252 66-25 61.47 COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, C, C, C, C, C, C, C, C, C, C, C, C, C,	⋖		125	250	1e-24			65.37	COAGULATION FACTORS IX/X-BINDING PROTEIN:	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR
252 6e-25 61.47 COAGULATION FACTORS IXX-BINDING PROTEIN; CHAIN: A, B, C, D, E, F; CHAIN: A, B, C, D, E, F; NULL 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; BCR-28 1.5e-30 0.60 0.60 WHC CLASS I H-2DD HEAVY CHAIN; CHAIN: CHAIN: CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: C, D; CHAIN: P; LY494; CHAIN: C, D; CHAIN: P; LY494; CHAIN: C, D;									CHAIN: A, B, C, D, E, F;	BINDING, C-TYPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD MOTIF 1 OOP FYCHANGED DIMER
126 252 3e-25 66.78 LITHOSTATHINE; CHAIN: A; B, C, D, E, F; NULL NULL NULL NULL NULL NULL NULL NUL	В		125	252	6e-25			61.47	COAGULATION FACTORS	COAGULATION FACTOR BINDING
126 252 3e-25 66.78 LITHOSTATHINE; CHAIN: 114 252 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; 114 252 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; 115 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: C, D; CHAIN: P; LY494; CHAIN: C, D;									IXX-BINDING PROTEIN;	IXX-BP COAGULATION FACTOR
126 252 3e-25 66.78 LITHOSTATHINE; CHAIN:  114 252 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A;  114 252 3e-28 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: CHAIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: C, D; CHAIN: P; LY49A; CHAIN: C, D;									CHAIN: A, B, C, D, E, F;	BINDING, C-1 YPE LECTIN, GLA- DOMAIN 2 BINDING, C-TYPE CRD
126   252   3e-25     66.78     LITHOSTATHINE; CHAIN: NULL   114   252   3e-28   0.75   0.86   LITHOSTATHINE; CHAIN: A;   114   252   3e-28   74.13   LITHOSTATHINE; CHAIN: A;   123   253   1.5e-30   0.60   0.60   MHC CLASS I H-2DD HEAVY   CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE   GLYCOPROTEIN 120 PEPTIDE;   CHAIN: P; LY49A; CHAIN: C, D;									· · · · · · · · · · · · · · · · · · ·	MOTIF, LOOP EXCHANGED DIMER
114 252 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; 114 252 3e-28 74.13 LITHOSTATHINE; CHAIN: A; 123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;			126	252	3e-25			82.99	LITHOSTATHINE; CHAIN:	PANCREATIC STONE INHIBITOR
114 252 3e-28 0.75 0.86 LITHOSTATHINE; CHAIN: A; 114 252 3e-28 74.13 LITHOSTATHINE; CHAIN: A; 123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN; CHAIN: CHAIN: CHAIN: CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;									NOTE	LECTIN
114 252 3e-28 74.13 LITHOSTATHINE; CHAIN: A; 123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	~		114	252	3e-28	0.75	98.0		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN
114 252 3e-28 74.13 LITHOSTATHINE; CHAIN: A; 123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;										PANCREATIC STONE PROTEIN, PSP;
114 252 3e-28 74.13 LITHOSTATHINE; CHAIN: A; 123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;										PANCREATIC STONE INHIBITOR, LITHOSTATHINE
123 253 1.5e-30 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;		_	114	252	3e-28			74.13	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN
123 253 1.5e-30 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;										PANCREATIC STONE PROTEIN, PSP;
123 253 1.5e-30 0.60 0.60 MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;					<u></u>					PANCREATIC STONE INHIBITOR,
CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	$\perp$		123	253	1.5e-30	0.60	0.60		MHC CLASS I H-2DD HEAVY	COMPLEX (NK RECEPTOR/MHC
., 5									CHAIN; CHAIN: A; BETA-2-	CLASS I) H-2 CLASS I
A 120 PEPTIDB; A; CHAIN: C, D;									MICROGLOBULIN; CHAIN: B;	HISTOCOMPATIBILITY ANTIGEN,
									HIV ENVELOPE	BZM; NK-CELL SURFACE
									CHAIN: P. I VAGA: CHAIN: C. D.	GLICOFROIEIN IE1/46, INCCELL, INHIBITOR VECEPTOR MHC.I.C.
HISTOCOMPATIBILITY, B2M, LY									, , , , , , , , , , , , , , , , , , ,	TYPE LECTIN-LIKE, 2
										HISTOCOMPATIBILÍTY, B2M, LY49,

PDB annotation		COMPLEX (NK RECEPTORMHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,	B2M; NK-CELL SURFACE	GLYCOPROTEIN YEI/48, NK CELL,	TYPE LECTIN-LIKE, 2	HISTOCOMPATIBILITY, B2M, LY49, LY-49	LECTIN SUB-MBP-C; 1RDL 9 C-TYPE	LECTIN, CALCIUM-BINDING PROTEIN IRDL 20				ANTIFREEZE PROTEIN	RECOMBINANT SEA RAVEN	PROTEIN, SOLUTION BACKBONE FOLD. C- 2 TYPE LECTIN	ANTIFREEZE PROTEIN						LECTIN CL-QPDWG; 1AFB 7 C-TYPE	LECTIN, CALCIUM-BINDING PROTEIN 14FR 22	SUGAR BINDING PROTEIN C-TYPE	LECTIN, CRD, SP-D, COLECTIN,	ALPHA-HELICAL COILED- 2 COIL,	LUNG SURFACTANT, SUGAR
Coumpound		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B;	HIV ENVELOPE	GLYCOPROTEIN 120 PEPTIDE; CHAIN: P. 1 V49A: CHAIN: C. D.	Circles 1, 5149A, Chain. C, D,		MANNOSE-BINDING PROTEIN-	C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN MANNOSE-BINDING	PROTEIN A (CLOSTRIPAIN	FRAGMENT) (CL-MBP-A) IRTM 3 IRTM 96	SEA RAVEN TYPE II	ANTIFREEZE PROTEIN; CHAIN:	A;		LECTIN MANNOSE-BINDING	PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3	CALCIUM AND	GLYCOPEPTIDE 2MSB 4		MANNOSE-BINDING PROTEIN-	A; IAFB 4 CHAIN: 1, 2, 3; IAFB 5	LUNG SURFACTANT PROTEIN	D; CHAIN: A, B, C;		
SEQFOL	D score						61.44	1	63.45							61.86					60.17					
PMF	score	0.43										0.41											0.83			
Verify	score	0.81										0.52											0.35			
Psi Blast		1.3e-27					1.2e-26		4.5e-23			1.3e-29				1.3e-25				;	1.5e-21	-	3e-31			
END	AA	253					251		252			250				251				,	291		288			
STAR	TAA	130					136		68			123				136			,,,,,,,		127		157			
CHAI		D							1			Ą				4					_		A			
PDB	a	1903					lrdľ		Irtm			2afp				2msb					latb		1508			
SEQ	NO:	1802					1802		1802			1802				1802					1803		1803			

									<del></del>				
PDB annotation	BINDING PROTEIN	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING HETERODIMER	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS	MEMBRANE PROTEIN SP-A; SP-A:PHOSPHOLIPID MOLOLAYER COMPLEX	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD	SIGNALING PROTEIN HEPATIC LECTIN H1; C-TYPE LECTIN CRD	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE	(AIM), BA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE
Coumpound		CD94; CHAIN: NULL;	CD94; CHAIN: NULL;	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN: B;	COAGULATION FACTOR IX- BINDING PROTEIN A; CHAIN: A: COAGULATION FACTOR IX-	B; CHAIN:	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	SURFACTANT PROTEIN A; CHAIN: A;	ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	
SEQFOL D score		73.97		68.01									
PMF score			86'0			0.48		-0.06	0.18	0.46	1.00	0.65	
Verify score		!	0.57			0.16		0.38	0.06	0.13	0.47	0.79	
Psi Blast		4.56-29	4.5e-29	16-24		1e-24		4.5e-24	1.2e-27	4.8e-25	1.5e-28	1.5e-27	
END		292	290	289		288		290	288	288	289	289	
STAR T AA		162	165	164		165	·	165	142	165	165	164	
CHAI N ID				A		A		В	A	A	A	A	
PDB ID		1b6e	1666	1bj3		Ejq1		1c3a	1du8	1dv8	ldv8	1e87	
SEQ ID NO:		1803	1803	1803		1803		1803	1803	1803	1803	1803	

			[7]							464	•	~	-				٠,	_,			_	ر,	-11				~						
PDB annotation		LECTIN-LIKE, 2 NKD, KLR	SUGAR BINDING PROTEIN C-TYPE I ECTIN MANNOSE RECEPTOR	C-TYPE LECTIN ALPHA-HELICAL	COILED-COIL 1HUP 12	C-TYPE LECTIN ALPHA-HELICAL	COILED-COIL 1HUP 12	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,	LECTIN	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN
Coumpound			MACROPHAGE MANNOSE RECEPTOR CHAIN A B	MANNOSE-BINDING PROTEIN:	1HUP 4 CHAIN: NULL; 1HUP 5	MANNOSE-BINDING PROTEIN;	1HUP 4 CHAIN: NULL; 1HUP 5	COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:	NULL		LITHOSTATHINE; CHAIN:	NULL	LITHOSTATHINE; CHAIN: A;
SEQFOL	D score			63.43	}			65.74										61.53													67.30		
PMF	score		0.95	}		0.40							0.48				ļ						0.48					68.0					0.86
Verify	score		0.62			0.33							0.32										0.38					0.77					0.75
Psi Blast			1.5e-25	3e-27	:	3e-27		1e-24					1e-24					6e-25					6e-25					3e-25			3e-25		3e-28
END	AA		288	288		589		585					288	-				291					290					291			291		291
STAR	TAA		165	150		164		164					165					164					165					165			165		153
CHAI	A ID		Ą					A					A					В					В										А
PDB	<b>a</b>		legg	Ihup	•	1hup		lixx					lixx		-			lixx					lixx					liit			llit		1qdd
SEQ	e ö		1803	1803		1803		1803					1803					1803					1803					1803			1803		1803

CHAI S	S	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
W T		٦.	\$		score	score	D score		PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR,
A 153 291		29	-	3e-28			73.96	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN PANCREATIC STONE PROTEIN, PSP., PANCREATIC STONE INHIBITOR,
C 162 292		29	2	1.5e-30	0.60	0.60		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I H1STOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YEI/48, NK CELL, NHIBITORY RECEPTOR, MHC-1, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,
D 169 292		292		1.36-27	0.81	0,43		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	LY-49 COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YEI/48, NK CELL, INHIBITORY RECEPTOR, MHC-1, C- TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,
175 290		29(		1.2e-26			61.70	MANNOSE-BINDING PROTEIN- C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20
176 289		28	9	1.2e-26	0.41	0.70		MANNOSE-BINDING PROTEIN. C; 1RDL 6 CHAIN: 1, 2; 1RDL 7	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20
127 291		53	_	4.5e-23			64.49	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM	

SEQ	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
NO:										
									3 1RTM 96	
1803	Zafp	¥	162	289	1.3e-29	0.52	0.41		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOLUTION BACKBONE FOLD, C- 2 TYPE LECTIN, ANTIFREEZE PROTEIN
1803	2msb	∢	175	290	1.3e-25			61.86	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	
1803	2msb	A	176	288	1.3e-25	0.57	0.54		LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	
1804	Iaui	B	-	80	4,8e-24	0.10	0.87		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1804	lcdm	<b>₹</b>	_	81	1.6e-29	-0.07	0.36		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE 11 ICDM 4	
1804	1cll			81	8e-36	-0.04	0.49		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
1804	1cmf		8	81	8e-32	0.23	0.60		CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1804	lexr	A	1	81	9.6e-34	0.11	0.93		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

PDB annotation		TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION			CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL
Coumpound		CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: NULL;	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCIUM BINDING PROTEIN CALMODULIN (TR=2=C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;
SEQFOL	D score								
PMF	score	0.89	1.00	0.95	0.98	0.98	1.00	0.99	0.98
Verify	score	0.39	0.23	0.25	0.52	0.30	0.60	0.58	0.57
Psi Blast		8e-30	1.6e-24	1.6e-24	1.4e-30	3.2e-35	8e-24	8e-24	6.4e-34
END	AA	81	81	81	81	82	250	250	227
STAR	I AA	14	1	-	12	1	114	114	44
CHAI		Ą			A	A	Y	ပ	A
PDB	3	1f71	Itef	1 top	Itrc	lvrk	1a9n	la9n	1d0b
SEQ	a ë	1804	1804	1804	1804	1804	1806	1806	1806

SEQ ID	PDB	CHAI	STAR T AA	END	Psi Blast	Verify	PMF score	SEQFOL D score	Coumpound	PDB annotation
NO:										
										ADHESION
1806	140b	A	25	235	1.3e-32	0.39	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1806	1dce	A	132	249	3.2e-25	0.51	0.99		RAB	TRANSFERASE CRYSTAL
									GERANYLGERANYLTRANSFE	STRUCTURE, RAB
									RASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFERASE,
									CHAIN: A, C; RAB	2.0 A 2 RESOLUTION, N-
									GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA
									KASE BETA SUBUNIT; CHAIN: B. D:	SOBUNII, BEIA SUBUNII
1806	1dce	A	84	207	3.2e-17	0.45	0.88		RAB	TRANSFERASE CRYSTAL
									GERANYLGERANYLTRANSFE	STRUCTURE, RAB
					•				RASE ALPHA SUBUNIT;	GERANYLGERANYLTRANSFERASE,
									CHAIN: A, C; RAB	2.0 A 2 RESOLUTION, N-
									GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA
									RASE BETA SUBUNIT; CHAIN:	SUBUNIT, BETA SUBUNIT
									B, D;	
1806	1ds9	А	111	191	3e-14	-0.40	0.78		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
									A;	RICH REPEAT, BETA-BETA-ALPHA
				-						CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1806	1ds9	A	125	251	1.6e-28	-0.60	0.46		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
									A;	RICH REPEAT, BETA-BETA-ALPHA
										CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1806	1ds9	A	73	179	3.2e-13	-0.30	0.01		OUTER ARM DYNEIN; CHAIN:	CONTRACTILE PROTEIN LEUCINE-
									A;	RICH REPEAT, BETA-BETA-ALPHA
_										CYLINDER, DYNEIN, 2
										CHLAMYDOMONAS, FLAGELLA
1809	1dkg	¥	250	398	0.0015	-0.10	0.11		NUCLEOTIDE EXCHANGE	COMPLEX (HSP24/HSP70) HSP70,
									FACTOR GRPE; CHAIN: A, B;	GRPE, MOLECULAR CHAPERONE,
									MOLECULAR CHAPERONE	NUCLEOTIDE EXCHANGE 2

PDB annotation	FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)			L- B-	HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE	HYDROLÁSE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLÁSE	HYDROLASE UTEROFERRIN, TRAP, PAP, TARTRATE RESISTANT ACID PURPLE ACID PHOSPHATASE, TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOENZYME, UTEROFERRIN, HYDROLASE	
Coumpound	DNAK; CHAIN: D;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	 PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;	II PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;
SEQFOL D score					61.74		63.06	
PMF		-0.07	0.07	0.28		0.34		0.52
Verify score		0.06	-0.12	0.21		-0.19		0.01
Psi Blast		3e-08	7.5e-13	1.6e-05	4.5e-10	4.5e-10	0.00014	1.5e-12
END		367	374	528	310	239	320	247
STAR T AA		143	102	439	32	39	28	10
CHAI N ID		В	А	4	А	Ą	∢	A
PDB ID		1dn1	1quu	lses	lqhw	Iqhw	lute	4kbp
SEQ ID NO:		1809	1809	1812	1814	1814	1814	1814

PDB annotation	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	METAL TRANSPORT MRP8, S100A8, CALGRANULIN A CALCIUM- BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHIBITORY FACTOR_RELATED PROTEIN 8, S100 PROTEIN		NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME
Coumpound	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP*UP* I IP*I IP*I IP*I IP*I IP*I IP*I IP*I	NUCLEOLIN RBD2; CHAIN: A;	MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score							
PMF score	0.46	0.12	0.21	0.13	0.55	0.31	0.18
Verify score	-0.30	-0.15	0.07	-0.32	0.29	0.31	-0.10
Psi Blast	3,2e-05	60-99.6	0.0045	3.2e-05	0.003	0.0093	6.4e-05
END AA	272	250	149	272	267	256	257
STAR T AA	195	180	101	195	188	195	195
CHAI N ID	A	A	∢				V
PDB ID	1b7f	1fjc	1mr8	1sxl	2u1a	2u1a	3sxl
SEQ ID NO:	1815	1815	1815	1815	1815	1815	1815

		D, TOR	D, TOR	<b></b>	ASE,	-	RON	RON		FE-	ਜ੍ਹ >		편 ^	
g	N.	IER, SE FOL 2 INHIB.	IER, ASE FOL 2 INHIB	ILY MAIN, 2 HELE	LOGEN		FUR FUR	FUR FUR	IRON.	r TWO 4	GENAS ECTRO		GENAS	
PDB annotation	NSATIC	MODIN TDROLA UREA	MODIN TDROLA UREA	D-FAM RE DOI SITE, 5-	Е DЕНА		NSPORT	NSPORT	NSFER ( N)	NSPORT	HYDRC 3553, EL PLEX		HYDRC 353, EL PLEX	
PDB a	COMPE	ASE HOETA HY	ASE HO ETA HY ITUTED	ASE HA ETA CC NDING	GENASI ASE		N TRA	N TRA	N TRA	N TRA	ENASE ROME (		ENASE ROME (	
	DOSAGE COMPENSATION	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE HAD-FAMILY ALPHA/BETA CORE DOMAIN, MG(II) BINDING SITE, 5-2 HELIX BUNDLE	DEHALOGENASE DEHALOGENASE, HYDROLASE		ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSFER (IRON- SULFUR PROTEIN)	ELECTRON TRANSPORT TWO 4FE- 4S CLUSTERS	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX		HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX	
				[1]	1 14					1		ы ы		— 円 ヴ
P		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	PHOSPHONOACETALDEHYDE HYDROLASE; CHAIN: A, B, C, D;	HAIN:		7-FE FERREDOXIN; CHAIN: NULL;	7-FE FERREDOXIN; CHAIN: NULL;	FERREDOXIN; ICLF 5 CHAIN: NULL 1CLF 6	XIIN;	FEJ-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FEJ- HYDROGENASE (SMALL	SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E	[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A, [FE]- HYDROGENASE (SMALL	SUBUNIT); CHAIN: D; CYTOCHROME C553; CHAIN: E
Coumpound		DROLA	DROLA	JACETA 3; CHALI	L-2-HALOACID DEHALOGENASE; CHAIN: NULL;		OXIN;	OOXIN;	N; ICLF	2[4FE-4S] FERREDOXIN; CHAIN: A	[FE]-HYDROGENASE (LAR SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL	SUBUNIT); CHAIN: D; CYTOCHROME C553;	[FE]-HYDROGENASE (LAR SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL	SUBUNIT); CHAIN: D; CYTOCHROME C553;
ပိ		CIDE HY	(IDE HY	SPHONC ROLASI	L-2-HALOACID DEHALOGENA NULL;		FERREI	FERREI	FERREDOXIN NULL 1CLF 6	:-4S] FEI N: A	HYDRO JNIT); C ROGEN,	JOHED); C	HYDRO JNIT); C	JNIT); C )CHRO
		EPOX A, B;	EPOX A, B;	PHOS HYDI D;	L-2-HA DEHAI NULL;		7-FE FE NULL;	7-FE   NULL	PERR	2[4FE-4S] CHAIN: A	FEJ-I SUBL HYDI	SUBU	SUBU HYDE	
SEQFOL D score		•												
PMF score		-0.14	0.05	0.64	-0.19		-0.19	-0.17	-0.17	-0.12	1.00		1.00	
Verify		-0.00	-0.84	0.20	0.12		0.05	0.17	0.43	0.53	0.37		0.23	
Psi Blast		3.2e-09	0.006	9e <b>-</b> 06	3e-10		8e-14	1.1e-10	1.1e-10	1.6e-11	6.4e-68		3e-92	
END P														
		305	69	143	316		219	254	199	200	519		504	
STAR T AA		172	39	38	28		137	176	137	137	136		173	-
CHAI N ID		⋖	æ	Ą						∢	<b>V</b>		A	
PDB ID		1ek1	lek1	l fez	lzm		1bc6	1bc6	1clf	1dur	1e08		1e08	
SEQ ID NO:		1819	1819	1819	1819		1820	1820	1820	1820	1820		1820	

ation				NLY	AY	', HYDROGENE	IPLASM	NLY	AY	, HYDROGENE	IPLASM		NLY AY	', HYDROGENE	IPLASM	IN TWO	IN, ALPHA	GION, 22	OILED-COILS,	NIS	IN TWO	IN, ALPHA	GION, 22	ILED-COILS,	NI:	EIN TRIPLE-	N	EIN TRIPLE-
PDB annotation		OXIDOREDUCTASE OXIDOREDUCTASE	OXIDOREDUCTASE OXIDOREDUCTASE	HYDROGENASE FE-ONLY	HYDROGENASE, X-RAY	CRYSTALLOGRAPHY, HYDROGENE	2 METABOLISM, PERIPLASM	HYDROGENASE FE-ONLY	HYDROGENASE, X-RAY	CRYSTALLOGRÁPHY, HYDROGENE	2 METABOLISM, PERIPLASM		HYDROGENASE FE-ONLY HYDROGENASE. X-RAY	CRYSTALLOGRAPHY, HYDROGENE	2 METABOLISM, PERIPLASM	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 2 2	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	I ANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE-	HELIX COILED COIL, CONTRACTII E PROTEIN	CONTRACTILE PROTEIN TRIPLE
Coumpound		PERIPLASMIC HYDROGENASE 1; CHAIN: A;	PERIPLASMIC HYDROGENASE I; CHAIN: A;	FE-ONLY HYDROGENASE	(SMALLER SUBUNIT); CHAIN:	S, T; FE-ONLY HYDROGENASE	(LARGER SUBUNIT); CHAIN: L,	FE-ONLY HYDROGENASE	(SMALLER SUBUNIT); CHAIN:	S, T; FE-ONLY HYDROGENASE	(LARGER SUBUNIT); CHAIN: L,	M;	FE-ONLY HYDROGENASE (SMALLER SUBUNIT): CHAIN:	S, T; FE-ONLY HYDROGENASE	(LARGER SUBUNIT); CHAIN: L, M:	ALPHA SPECTRIN; CHAIN: A,	B, C;				ALPHA SPECTRIN; CHAIN: A,	B, C;				HUMAN SKELETAL MUSCLE	ALPHA-ACTININ 2; CHAIN: A;	HUMAN SKELETAL MUSCLE
SEQFOL	D score	232.77		223.69																						52.84		
PMF	score		1.00					1.00					1.00 1.00			0.01					0.36							0.43
Verify	score		0.33		•			0.40	-				0.61			-0.18					-0.09							-0.34
Psi Blast		1.4e-85	1.4e-85	4.5e-92				3.2e-68					4.5e-92			6e-09					1.5e-07					9e-12		9e-12
END	ΨΨ	574	572	524				519					504			344	-1				207					302		340
STAR	TAA	1	69	117				122	_				173			104					[2]					54		56
CHAI	e Z	А	A	L				L								Ą					¥					V.		A
PDB	<u>e</u>	lfeh	1 feh	1hfe	**			Ihfe					lhfe			lcun	_			1	lcan			-		1dnn		lquu
SEQ	ΘÖ	1820	1820	1820				1820					1820			1821				,	1821					1821		1821

PDB annotation	HELIX COILED COIL.	CONTRACTILE PROTEIN	COMPLEX (BLOOD	AUTOPROTHROMBIN IIA; HYDROLASE, SERINE	PROTEINASE), PLASMA CALCIUM	BINDING, 2 GL I COFROTEIN, COMPLEX (BLOOD	COAGULATION/INHIBITOR)	ANTI-COAGULANT ANTI- COAGULANT PEPTIDIC	INHIBITORS, CONFORMATIONAL 2	FLEXIBILITY, SERINE PROTEASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA	OR OR	HYDROLASE INHIBITOR ALL-BETA	STRUCTURE, HYDROLASE INHIBITOR	BLOOD COAGULATION, SERINE	PROTEASE, COMPLEX, CO-FACTOR,		2 RECEPTOR ENZYME, INHIBITOR,	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	TOR ENZYME, INHIBITOR, IF, 3 COMPLEX (SERINE SE/COFACTOR/LIGAND)	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND) APOPTOSIS TRAIL, DR5, COMPLEX	TOR ENZYME, INHIBITOR, IF, 3 COMPLEX (SERINE SE/COFACTOR/LIGAND) SIS TRAIL, DR5, COMPLEX	TOR ENZYME, INHIBITOR, FF, 3 COMPLEX (SERINE SE/COFACTOR/LIGAND) SIS TRAIL, DR5, COMPLEX	TOR ENZYME, INHIBITOR, F, 3 COMPLEX (SERINE SE/COFACTOR/LIGAND) SIS TRAIL, DR5, COMPLEX
		$\neg \vdash$			PROTEI	COMPLI			INHIBIT	FLEXIBILIT	HYDRO	INHIBITOR	HYDRO	STRUCTUR			_								
Coumpound	ALPHA-ACTININ 2: CHAIN: A:		ACTIVATED PROTEIN C; CHAIN: C. 1.: D-PHE-PRO-MAI:	CHAIN: P;				HIRUSTASIN; CHAIN: NULL;			BOWMAN-BIRK TRYPSIN	INTERPRETATION &	BOWMAN-BIRK TRYPSIN	INHIBITOR; CHAIN: A	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L, H;	SOLUBLE TISSUE FACTOR;		CHAIN: T, U; D-PHE-PHE-ARG-	CHAIN: T, U; D-PHE-PHE-A CHLOROMETHYLKETONE	CHAIN: T, U; D-PHE-PHE-AR(CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	CHAIN: T, U; D-PHE-PHE-ARG CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C; DEATH RECEPTOR 5; CHAIN:	CHAIN: T, U; D-PHE-PHE-ARG CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C; DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED	CHAIN: T, U; D-PHE-PHE-1 CHLOROMETHYLKETONI (DFFRCMK) WITH CHAIN DEATH RECEPTOR 5; CHA A, B, C, G, H, I; TNF-RELA' APOPTOSIS INDUCING	CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C; DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;
SEQFOL	D score		51.57																						
PMF	score							-0.15			-0.03		-0.15		-0.19						0.10	-0.18	-0.18	-0.18	-0.18
Verify	score							1.12			0.53	!	0.87		0.56						00	1.08	1.08	1.08	1.08
Psi Blast			9e-08					6e-11			1.4e-26		1.5e-19		7.5e-13						11.03.17	7.5e-11	7.5e-11	7.5e-11	7.5e-11
END			125					113			165		126		135						7.7	77	77	77	77
STAR	TAA		29					45			36		4		2						C	2	7	2	2
CHAI	OI N		IJ								A		A		Ţ						<	A	Ą	A	A
EQ4	e		laut					1bx7			1c2a		1c2a		1dan						14113	1du3	1du3	1du3	1du3
SEQ	NO:		1822					1822			1822		1822		1822				_		1822	1822	1822	1822	1822

									_		_				_					
PDB annotation		APOPTOSIS TRAIL, DR5, COMPLEX	SERINE PROTEINASE COAGULATION FACTOR II;	FETOMODULIN, TM, CD141	ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX	PLANT PROTEIN TWO	HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO	HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO	HOMOLOGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA,	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA;	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,
Coumpound	APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND: CHAIN: D, E, F, I, K, I.:	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN: CHAIN: M N	O, P; THROMBOMODULIN;	CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-	ARM; CHAIN: E, F, G, H;	AGGLUTININ ISOLECTIN VI;	CHAIN: A	AGGLUTININ ISOLECTIN VI;	CHAIN: A	AGGLUTININ ISOLECTIN VI;	CHAIN: A	AGGLUTININ ISOLECTIN	VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN	VI/AGGLUTININ ISOLECTIN V;	CHAIN: A;	AGGLUTININ ISOLECTIN	CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;
SEQFOL D score																				
PMF		-0.15	-0.14				-0.18		-0.12		0.16		0.17		-0.11			0.10		-0.17
Verify score		1.17	0.58				0.49		1.11		1.00		0.87		1.02			1.08		0.24
Psi Blast		6e-12	4.5e-11				1.4e-18		7.5e-19		1.4e-18		1.5e-19		1.2e-19		;	1.5e-19		7.5e-17
END AA		96	155				1111		91		141		121		06			141		160
STAR T AA		6	47	· · · · · ·			12		4		52		19		4			52		75
CHAI N ID		Ą	Ţ				A		٧		A		A		A			∢		А
PDB ID		1du3	1dx5				1ehd		1ehd		lehd		leis		1eis			leis		1eis
SEQ ID NO:		1822	1822				1822		1822		1822		1822		1822			1822		1822

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ÿ	9		T AA	AA		score	score	D score		
									CHAIN: A;	SUPERANTIGEN
1822	len2	Ą	12	121	3e-18	0.40	-0.13		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE
1822	len2	A	2	06	6e-16	1.10	-0.18		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	len2	A	52	141	3e-21	1.04	0.11		AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	len2	A	62	160	6e-18	0.61	-0.14		AGGLUTININ ISOLECTIN 1/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1822	lext	A	10	177	7.5e-20			62.34	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	lext	Ą	12	175	7.5e-20	0.78	-0.14		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	lext	¥	co.	128	6e-13	0.63	-0.14		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1822	ligr	¥.	4	178	1.5e-28	0.40	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1822	1klo		47		1.2e-19	0.65	-0.15		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	1klo		4	155	7.5e-27	1.13	-0.06	02.00	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1822	Incf	A	34		1.5e-12			50.41	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8

			T	г	I	
PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	EXTRACELLULAR MODULE OSTEONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Coumpound	B; INCF 5	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	BASEMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D. PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score					55.26	
PMF score		-0.14	-0.19	-0.20		-0.20
Verify score		0.68	0.10	0.14		0.44
Psi Blast		1.5e-12	6e-26	3e-23	3e-23	9e-14
END AA		155	171	179	178	123
STAR T AA		35	12	19	36	εn .
CHAI N ID		A	A	i.	H	ı,
PDB ID		Incf	Inub	lpfx	lpfx	1pfx
SEQ ID NO:		1822	1822	1822	1822	1822

			-								_	- 7	_								_							
PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	STRUCTURE. FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SEATING FRO LEASE INHIBITOR FACTOR XA INHIBITOR	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA   INHIBITOR, 2 SERINE PROTEASE
Coumpound			ANTISTASIN; CHAIN: NULL;				THE TALLED THE CHOICE	ANTISTASIN; CHAIN: NOLL;					ANTISTASIN; CHAIN: NULL;				,		ANTISTASIN; CHAIN: NULL;		,				ANTISTASIN; CHAIN: NULL;			
SEQFOL D score																			63.90									
PMF score			0.54					00.0-					0.11												-0.12			
Verify score			0.63			•	0.51	/c.o					0.03												0.61			
Psi Blast			1.2e-18				0.0	1.35-21			,		7.5e-25	-					7.5e-25						1.5e-18			
END AA			134				143	<u>+</u>				ļ	176						180						117			
STAR T AA			22				42	<del>}</del>					71						71						∞			
CHAI N ID																												
PDB ID			1skz				1-1-1	Zwei					1skz						Iskz						1skz			
SEQ ID NO:			1822				0001	7701					1822						1822		_				1822		_	

PDB annotation	INHIBITOR, THROMBOSIS			ANTI-COAGULANT ANTI- COAGULANT, PEPTIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHIBITOR	APOPTOSIS TRAIL, DR5, COMPLEX					BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
Coumpound		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	HIRUSTASIN; CHAIN: NULL;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) IMHUA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MHUA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (/NMR\$) 1MRTA 2	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMR\$) 1MRTA 2	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score		107.39					65.07		63.47	
PMF			0.03	0.07	-0.12	1.00		1.00		0.10
Verify			0.57	0.23	0.07	0.40		0.49		0.34
Psi Blast		6e-30	3e-26	4.5e-20	3e-08	9e-16	9e-16	9e-16	9e-16	7.5e-06
END		158	160	107	107	108	108	108	108	106
STAR T AA		2	2	50	49	82	78	78	78	54
CHAI N ID		A	А		A					T
PDB ID		9wga	9wga	1bx7	1du3	1mhu	1mhu	Imrt	1mrt	1xka
SEQ ID NO:		1822	1822	1824	1824	1824	1824	1824	1824	1824

					LB;		LB;					•				ъį. 			-	_	 ——		ري.		Ή,
ion					CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID	BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB;	BINDING PROTEIN, 2 CALCIUM-	TRANSCRIPTION REGULATION	UCLEAR	EMIA, 2	TRANSCRIPTION REGULATION	TOSIS	SYNAPTOTAGMIN, C2-DOMAIN,		NEUROTRANSMITTER 2 RELEASE,	IOSIS	TOSIS	SYNAFIOIAGMIN, CZ-DOMAIN, EVOCVTORIS		NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS		PHOSPHOLIPASE, LIPID-BINDING,		HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING,
PDB annotation					IDING PR HOSPHO	TEIN, 2 C TEIN	DING PR	TEIN, 2 C	ON REGI	GENE, N	3), LEUKI	ON REGI	S/EXOCY	MIN, C2-		MITTER	S/EXOCY	S/EXOCY	MIN, CZ-		MITTER S/EXOCY	CPLA2;	SE, LIPII		CPLA2; SE, LIPII
PD					CALCIUM-BINDING PROTEI CALCIUM++/PHOSPHOLIPIE	BINDING PROTEIN BINDING PROTEIN	CALCIUM-BINDING PROTEI	BINDING PROTEIN	SCRIPTI	PROTO-ONCOGENE, NUCLEAR	BODIES (PODS), LEUKEMIA, 2	SCRIPTI	ENDOCYTOSIS/EXOCYTOSIS	PTOTAG	EXOCYTOSIS,	COTRANS	ENDOCY I OSIS/EXOCY I OSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAFIOIAG	i Losis,	NEUROTRANSMITTER 2 RELI ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2	PHOLIPA	HYDKOLASE	HYDROLASE CPLA2; PHOSPHOLIPASE, LII
					CALC		CALC		TRAN	PROT	BODI	TRAD	END	SYN	EXOC	NEUF PARTIE		FNDC	NAN	באלם !	NEOR	HYDI	PHOS	НХП	PHOS
		OFORM	)FORM		TA);		TA);		J. J.				AIN: A;				4 171 4	AIN: A;				IPASE			IPASE
Coumpound		NEIN NEIN IS	NEIN NEIN IS		SE C (BE		SE C (BE		N FACT	ULL;			AIN I; CF				TO I LOI	AIN I; CF				OSPHOL	÷		OSPHOL s;
Coun		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3		PROTEIN KINASE C (BETA); CHAIN: A, B;		PROTEIN KINASE C (BETA);	<u> </u>	TRANSCRIPTION FACTOR	PML; CHAIN: NULL;			SYNAPTOTAGMIN I; CHAIN: A;				TOTACT	STNAFIOIAGMIN I; CHAIN: A;				CYTOSOLIC PHOSPHOLIPASE	A2; CHAIN: A, B;		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;
		METALL METALL II 4MT2 3	METALL( METALL( II 4MT2 3		PROTEIN KIN CHAIN: A, B;		PROTEIN KIN		TRANS	PML; C			SYNAP				G V V V V	SYNAR				CYTOS	A2; CH.	1	CYTOS A2; CH
SEQFOL	D score		127.57																-						
PMF 8	score	0.15		'	00.1		0.90	_	0.13				1.00				90	0.98				0.01		0	0.28
Verify	score																1			-		•			
	SC	-0.09			0.47		0.27	. <u>-</u>	0.33				0.68				0.00	0.70				0.17		0	0.37
Psi Blast		1.3e-14	1.3e-14		4.8e-42		3.2e-37		0.00075				3.2e-46				1 40 07	1.46-27				1.1e-12		1	1.2e-15
END	AA	108	108		491		646		109				484				620	650				480		30,	639
STAR	TAA	48	48		355		528		09				355				510	010				366		, 6,	9750
CHAI	ON N				∢		A						٧					4				Ą			A
PDB	e	4mt2	4mt2		1a25		1a25	-	Ibor				1byn				Them	toyn				1cjy			ıcjy
SEQ	B Ö	1824	1824		1825		1825		1825				1825				1825	707				1825		2001	1825

SEQ PDB	B CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation	
		I AA	AA		score	score	D score			
									HYDROLASE	
1825 Idjx	k A	370	467	4.5e-15	0.19	0.62		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C. CHAIN: A.	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER	
								B;	HYDROLASE, HYDROLASE, LIPID	
									DEGRADATION, 2 TRANSDUCER,	
_									CALCIUM-BINDING,	
	_								PHOSPHOLIPASE C, 3	
$\dashv$									PHOSPHOINOSITIDE-SPECIFIC	
1825   1djx 	¥ _	526	620	6e-13	-0.07	0.12		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN; A,	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER	
								B;	HYDROLASE, HYDROLASE, LIPID	
									DEGRADATION, 2 TRANSDUCER,	
	_								CALCIUM-BINDING,	
									PHOSPHOLIPASE C, 3	
-	-								PHOSPHOINOSITIDE-SPECIFIC	
1825   1djx	ж —	370	467	4.5e-15	0.16	0.58		PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1;	
								PHOSPHOLIPASE C, CHAIN: A,	PHOSPHORIC DIESTER	
								B;	HYDROLASE, HYDROLASE, LIPID	
									DEGRADATION, 2 TRANSDUCER,	
	_								CALCIUM-BINDING,	
									PHOSPHOLIPASE C, 3	
$\dashv$	$\dashv$								PHOSPHOINOSITIDE-SPECIFIC	
1825   1dqv	<b>V</b>	357	649	3.2e-88	0.47	1.00	-	SYNAPTOTAGMIN III; CHAIN:	ENDOCYTOSIS/EXOCYTOSIS BETA	
	-							A;	SANDWICH, CALCIUM ION, C2	
$\dashv$	+								DOMAIN	
1825   1dqv	Α 	512	671	4.8e-33	0.24	0.46		SYNAPTOTAGMIN III; CHAIN:	ENDOCYTOSIS/EXOCYTOSIS BETA	
								A;	SANDWICH, CALCIUM ION, C2	
-	+								DOMAIN	
1825   1dsy	A A	354	494	1.3e-45	0.33	96.0		PROTEIN KINASE C, ALPHA	TRANSFERASE CALCIUM++,	
								TYPE; CHAIN: A;	PHOSPHOLIPID BINDING PROTEIN,	
									CALCIUM-BINDING 2 PROTEIN,	
				****					PHOSPHATIDYL SERINE, PROTEIN	
+				1					KINASE C	
1825   1dsy	уА	510	650	6.4c-40	0.38	0.31		PROTEIN KINASE C, ALPHA	TRANSFERASE CALCIUM++,	

	T								
PDB annotation	PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN 1; RAG1, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINUCLEAR CLUSTER, ZINC	FINGER, DNA-BINDING PROTEIN			TRANSPORT PROTEIN FYVE DOMAIN, ENDOSOME
Coumpound	TYPE; CHAIN: A;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	PHOSPHOLIPASE A2; CHAIN: NULL;	PHOSPHOLIPASE A2; CHAÏN: NULL;	RAG1; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	DOMAIN) (CALB) IRSY 3 CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	PHOSPHATIDYLINOSITOL-3- PHOSPHATE BINDING FYVE
SEQFOL D score						81.61			
PMF score		0.10	0.41	0.23	0.03		1.00	96:0	0.16
Verify score		0.10	-0.18	0.31	0.21		0.81	0.48	0.04
Psi Blast		0.00045	1.5e-16	7.5e-17	0.003	4.8e-46	4.8e-46	1.6e-27	0.00075
END AA		109	480	631	109	483	482	636	91
STAR T AA		09	373	528	40	347	355	510	09
CHAI N ID		Ą			•				٧
PDB ID		1g25	lrlw	lriw	lrmd	Irsy	Irsy	lrsy	lvfy
SEQ ID NO:		1825	1825	1825	1825	1825	1825	1825	1825

PDB annotation	MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
Coumpound	CHAIN: A;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score			71.27			69.53	72.01
PMF score		69'0		1.00	0.58		
Verify score		0.40		0.62	0.53		
Psi Blast		36-22	3e-22	3.2e-29	1.4e-46	4.8e-53	1.1e-60
END AA		120	131	496	649	169	170
STAR T AA		01	∞	357	512	29	26
CHAI N ID		В	В	А	A		A
PDB UD		1zbd	1zbd	3rpb	3rpb	1011	lvrk
SEQ ID NO:		1825	1825	1825	1825	1828	1828

PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
Coumpound	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	BLOOD COAGULATION FACTOR VIIA; CHAIN: 1, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: I, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;
SEQFOL D score	58.73			60.57	1
PMF score		-0.17	0.96		0.99
Verify score		0.14	0.10		0.26
Psi Blast	1.3e-20	1.36-20	6.4e-16	1.5e-22	6.4e-16
END	145	202	231	193	231
STAR T AA	47	73	152	54	152
CHAI N ID	Ţ	H	ı	L	T
PDB ID	laut	laut	1dan	1dan	1dva
SEQ ID NO:	1833	1833	1833	1833	1833

		T				1					
PDB annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE COMPLEY PROTEASE COMPLEY	RECEPTOR ENZYME, 3 INHIBITOR, GLA, COMPLEX, COFFACTOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN GI YCOPROTEIN GI YCOPROTEIN	COMPLEX (BLOOD	CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,
Coumpound	FIBRILLIN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	CHAIN: T; 5L15; CHAIN: I;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	FACTOR IXA; CHAIN: C, L,; D-				FACTOR IXA; CHAIN: C, L.; D. PHE-PRO-ARG; CHAIN: I;
SEQFOL D score	56.72	54.06				70.82	64.61				
PMF score			1.00		0.43	<b>-0</b> .01				,	-0.12
Verify score			0.44		0.32	0.12					0.10
Psi Blast	1.3e-15	9e-14	6.4e-16		1e-28	1.1e-20	6e-35				6e-35
END	226	173	231		205	242	146				218
STAR T AA	149	10	152		43	52 S	22				54
CHAI N ID		A	Ţ				T				Г
PDB ID	lemn	1ext	1fak		1klo	1klo	1pfx				1pfx
SEQ ID NO:	1833	1833	1833		1833	1833	1833				1833

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PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
Coumpound		FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA
SEQFOL D score					55.94	
PMF score		0.07	0.62	0.98		0.18
Verify score		-0.16	0.07	0.30		0.04
Psi Blast		6 <del>c</del> ·29	1.5e-21	6.4e-15	7.5e-24	7.5e-24
END		226	226	231	561	207
STAR T AA		92	156	156	91	92
CHAI N ID		Ţ	J	J	J	Ы
PDB ID		lpfx	1qfk	lqfk	1qfk	1qfk
SEQ ID NO:		1833	1833	1833	1833	1833

PDB annotation			PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	
Coumpound		(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PHOSPHOLIPASE A2; CHAIN: A, B;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3
SEQFOL	D score							59.27		78.80
PMF	score		0.63	0.19	0.16	-0.12	0.64		90:0	
Verify	score		-0.02	0.27	0.23	0.03	0.18		0.32	
Psi Blast			1e-23	1e-23	3e-21	4.5e-18	3e-18	1,1e-21	1.16-21	7.5e-25
END	AA		226	125	196	130	226	208	207	207
STAR	TAA		137	43	72	34	156	91	92	28
CHAI	N B					A	1	T	ı	A
PDB	<b>a</b>		1tpg	1tpg	1tpg	1vap	1xka	1xka	Ixka	9wga
SEQ	e ö		1833	1833	1833	1833	1833	1833	1833	1833

PDB annotation	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	TRANSFERASE TYPE II DNA- (CYTOSINE N4) METHYLTRANSFERASE, AMINO 2 METHYLATION, SELENOMETHIONINE, MULTIWAVELENGTH ANOMALOUS 3 DIFFRACTION	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	RHODOPSIN; CHAIN: A, B	RHODOPSIN; CHAIN: A, B	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP* UP*UP*UP*UP-UP*U). CHAIN: P, Q;	N-4 CYTOSINE-SPECIFIC METHYLTRANSFERASE PVU II; CHAIN: A;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;
SEQFOL D score						
PMF	-0.07	0.10	0.36	0.27	0.24	-0.19
Verify score	0.11	-0.14	-0.03	-0.57	-0.34	0.05
Psi Blast	3e-20	7.5e-18	1.6e-19	4.5e-05	6.4e-23	3.2e-26
END	320	299	144	480	150	237
STAR T AA	4	착	19	433	59	75
CHAI N ID	A	В	A	¥	V	В
PDB ID	8811	1f88	1b7f	1500	1cvj	1evj
SEQ ID NO:	1834	1834	1835	1835	1835	1835

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Commonud	PDB annotation
ΑÖ	A	OI N	TAA	AA		score	score	D score	•	
1835	1d2h	A	424	492	1.2e-14	-0.57	0.17		GLYCINE N. METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1835	1d9a	А	72	144	3.2e-17	-0.02	0.16		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1835	Idus	A	421	567	9.6e-20	0.37	0.75		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1835	1fjc	A	73	139	1.3e-13	0.19	0.62		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1835	1g6q		402	580	3.2e-11	-0.51	0.03		HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1g6q	_	420	492	1.3e-13	0.20	0.83		HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1hd1	A	74	144	3.2e-23	0.27	0.06		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1835	1qam	A	410	592	6e-21	-0.06	0.58		ERMC' METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RRNA METHYLTRANSFERASE ERMC', COFACTOR ANALOGS
1835	Iqam	A	413	524	6.4e-05	-0.12	0.05		ERMC' METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RRNA METHYLTRANSFERASE ERMC', COFACTOR ANALOGS
1835	lvid		424	538	1.5e-15	0.23	0.66		CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION
1835	1xva	Ą	426	492	1.5e-10	-0.47	0.05		GLYCINE N- METHYL TRANSFERASE;	METHYLTRANSFERASE GNMT, S-ADENOSYL-L-METHIONINE):

SEQ ID	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
Ö									CHAIN: A, B;	GLYCINE METHYLTRANSFERASE
1835	2mss	A	74	144	4.8e-18	-0.04	0.00		MUSASHII; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1835	2sxl		73	152	8e-18	0.04	0.35		SEX-LETHAL PROTEIN; CHAIN: NULL;	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING
1835	3sx1	A	19	137	86-18	0.10	-0.05		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSA GE COMPENSATION
1836	1buo	A	4	85	3.2e-16	0.37	-0.05		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1836	1gof		204	505	1.6e <b>-</b> 06	-0.33	0.34		OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
1836	1gof		217	450	7.5e-13	-0.42	0.13		OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
1836	lgof		246	372	1.5e-15	-0.23	0.07		OXIDOREDUCTASE(OXYGEN( A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	
1837	1dan	7	285	370	4.8e-10	-0.00	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR,

	STAR END Psi Blast Verify PMF TAA AA score score	Psi Blast Verify PMF score	Blast Verify PMF score	PMF score		SEQFOL D score		Coumpound SOLUBLE TISSUE FACTOR;	PDB annotation 2 RECEPTOR ENZYME, INHIBITOR,
								CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
ldan L 361 449 1.1e-12 0.04 -0.20	449 1.1e-12 0.04	1.1e-12 0.04	12 0.04	<u></u>	-0.20			BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR,
								CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1dan L 530 583 3.2e-08 0.21 -0.20	583 3.2e-08 0.21	3.2e-08 0.21	0.21		-0.20			BLOOD COAGULATION FACTOR VIIA: CHAIN: L. H:	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX CO-FACTOR
,			,					SOLUBLE TISSUE FACTOR;	2 RECEPTO'R ENZYME, INHIBITOR,
								CHAIN: T, U; D-PHE-PHE-ARG-CHI OROMETHYI KETONE	GLA, EGF, 3 COMPLEX (SERINE PROTE A SE/COEA CTOR // 1GA ND)
								(DFFRCMK) WITH CHAIN: C;	
1dva L 285 370 4.8e-10 0.09 -0.20	370 4.8e-10 0.09	4.8e-10 0.09	60.0		-0.20			DES-GLA FACTOR VIIA	HYDROLASE/HYDROLASE
								(HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT	INHIBITOR PROTEIN-PEPTIDE COMPLEX
								CHAIN); CHAIN: L, M; (DPN)-	Com the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
								PHE-ARG; CHAIN: C, D; PEPTIDE E-76: CHAIN: X. Y:	
1dva L 361 449 1.1e-12 0.10 -0.19	449 1.1e-12 0.10	1.1e-12 0.10	.12 0.10		-0.19		<del>!</del>	DES-GLA FACTOR VIIA	HYDROLASE/HYDROLASE
								(HEAVY CHAIN); CHAIN: H, I;	INHIBITOR PROTEIN-PEPTIDE
								CHAIN); CHAIN: L, M; (DPN)-	
								PHE-ARG; CHAIN: C, D;	
				1			-	PEPTIDE E-76; CHAIN: X, Y;	
Idva L 530 583 3.2e-08 0.27 -0.20	583   3.2e-08   0.27	3.2e-08 0.27	0.27		-0.20			DES-GLA FACTOR VIIA	HYDROLASE/HYDROLASE
								DES-GLA FACTOR VIIA (LIGHT	COMPLEX
			-		_			CHAIN); CHAIN: L, M; (DPN)-	
								PHE-ARG; CHAIN: C, D;	
							$\dashv$	PEPTIDE E-76; CHAIN: X, Y;	

PDB annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MÁTRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE
Coumpound	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN; NULL;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;
SEQFOL D score						
PMF score	-0.19	-0.17	-0.20	-0.20	-0.20	-0.20
Verify score	0.19	0.07	0.03	0.03	0.13	0.22
Psi Blast	1.4e-10	3.2e-09	4.8e-09	1.6e-11	4.8e-09	3.2e-08
END AA	185	227	583	182	221	583
STAR T AA	107	149	530	102	143	530
CHAI N ID				A	A	1
PDB ID	lemn	lemn	lemn	1f5y	1f5y	1fak
SEQ ID NO:	1837	1837	1837	1837	1837	1837

STAR END Psi Blast Verify PMF SEQFOL Coumpound TAA AA score score D score
SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;
328 409 1.1e-12 0.22 -0.13 FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: 1;
361 449 1.6e-11 0.16 -0.19 FACTOR IXA; CHAIN: C, L.; D-PHE-PRO-ARG; CHAIN: I;
152 243 4.8e-10 0.03 -0.15 COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C; CHAIN: C;
365 449 6.4e-12 0.02 -0.19 COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C; CHAIN: C;
530 583 3.2e-08 0.08 -0.20 COAGULATION FACTOR VIIA

PDB annotation	BLOOD COAGULATION, SERINE PROTEASE		BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	<del> </del>	T	HYDROLASE HYDROLASE, NAD BINDING PROTEIN	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
Coumpound	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I 1VMO 3	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	S-ADENOSYLHOMOCYSTEINE HYDROLASE; CHAIN: A, B;	TROPINONE REDUCTASE-I; CHAIN: A, B;
SEQFOL D score								
PMF score		-0.19	-0.20	-0.20	-0.14	-0.14	0.00	0.21
Verify score		0.19	0.22	0.04	0.21	0.01	-0.09	0.34
Psi Blast		3e-15	1.6e-08	4.8e-11	9.6e-16	4.8e-16	0.0032	0.00064
END		470	585	158	403	476	207	215
STAR T AA		303	530	73	250	275	163	173
CHAI N ID		A	L)	J	A	A	A	∢
PDB ID		lvmo	lxka	Ixka	9wga	9wga	1a7a	lael
SEQ US US US US US US US US US US US US US		1837	1837	1837	1837	1837	1838	1838

							7.			
PDB annotation		OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE	OXIDOREDUCTASE NAD- DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB	OXIDOREDUCTASE AMINO ACID DEHYDROGENASE, OXIDATIVE DEAMINATION MECHANISM, 2 OXIDOREDUCTASE	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1CDO 15	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1CDO 15	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE	ASE RETINOL ASE, GASTRIC MAANN OR FOLD	ASE RETINOL ASE, GASTRIC MAANN OR FOLD	OXIDOREDUCTASE BETA1 ADH; 1DEH 9 NAD+ DEPENDENT
PDB		OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TROPINE, SHORT-CHAIN DEHYDROGENASE	OXIDOREDUCTASE NAD- DEPENDENT OXIDOREDI SHORT-CHAIN ALCOHOL DEHYDROGENASE, PCB DEGRADATION	OXIDOREDUCTASE DEHYDROGENASE, DEAMINATION MEC	OXIDOREDUCTASE (CH-OH(D) NAD(A)) OXIDOREDUCTASE 1C 15	OXIDOREDUCTASE (CH-OH(D)- NAD(A)) OXIDOREDUCTASE 1C 15	OXIDOREDUCTASE DEHYDROGENASE, OXIDOREDUCTASE	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINUCLEOTIDE FOLD	OXIDOREDUCTASE RETINOL DEHYDROGENASE, GASTRIC ALCOHOL ROSSMANN OR DINIICI FOTTIDE FOILD	OXIDOREDUCTASE BETAI IDEH 9 NAD+ DEPENDENT
Coumpound		TROPINONE REDUCTASE-I; CHAIN: A, B;	CIS-BIPHENYL-2,3- DIHYDRODIOL-2,3- DEHYDROGENASE; CHAIN: NULL;	L-PHENYLALANINE DEHYDROGENASE; CHAIN: A; L-PHENYLALANINE DEHYDROGENASE; CHAIN: B;	ALCOHOL DEHYDROGENASE; 1CDO 6 CHAIN: A, B; 1CDO 7	ALCOHOL DEHYDROGENASE; ICDO 6 CHAIN: A, B; 1CDO 7	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	ALCOHOL DEHYDROGENASE CLASS IV SIGMA CHAIN; CHAIN: A, B, C, D;	HUMAN BETAI ALCOHOL DEHYDROGENASE; 1DEH 7
SEQFOL D score	2000				56.21			64.19		
PMF	3COI C	0.05	0.25	0.89		1.00	0.03		1.00	1.00
Verify	21026	0.44	-0.07	0.67		0.64	0.19		0.81	0.63
Psi Blast		0.00064	4.8e-05	0.00013	1.3e-76	1.3e-76	3.2e-05	4.8e-75	4.8e-75	3.2e-81
END	A.C.	215	222	221	367	366	261	367	366	366
STAR	. na	173	173	173	-	25	173	-	26	25
CHAI		Ф		Ą	Ą	Y	⋖	Ą	Ą	A
PDB	1	lae1	1bdb	lc1d	1cdo	1cdo	1cyd	1d1t	ldlt	Ideh
SEQ	NO:	1838	1838	1838	1838	1838	1838	1838	1838	1838

Fsi Blast
1.6e-69 0.77
4.8e-77 0.73
_
9.6e-07 -0.03
1.6e-51
1
1.6e-51 0.59
0.28
0.75

PDB annotation		OXIDOREDUCTASE GLUTATHIONE- DEPENDENT FORMALDEHYDE DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL	DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE DEHYDROGENASE	OXIDOREDUCTASE GLUTATHIONE-	DEHYDROGENASE, NAD+ DEPENDENT ALCOHOL	DEHYDROGENASE 2	GLUTATHIONE DEPENDENT	DEHYDROGENASE	TRANSFERASE	(METHYLTRANSFERASE) COMT;	TRANSFERASE,	METHYLTRANSFERASE,	NEUROTRANSMITTER DEGRADATION	$\vdash$	7		, OXIDOREDUCTASE	OXIDOREDUCTASE	, OXIDOREDUCTASE		KINASE KINASE, SIGNAL
Coumpound	1QOR 3	HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A, B;		HUMAN CHICHI ALCOHOL DEHYDROGENASE; CHAIN: A,	B;				CATECHOL O-	METHYL TRANSFERASE;	CHAIN: NULL;			TRIHYDROXYNAPHTHALENE	REDUCTASE; CHAIN: A, B;	NADP-DEPENDENT ALCOHOL	DEHYDROGENASE; CHAIN: A,   B. C, D;	NADP-DEPENDENT ALCOHOL	DEHYDROGENASE; CHAIN: A,	B, C, U;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;
SEQFOL D score		72.11														52.30					52.68
PMF				1.00					0.47					0.49				1.00			
Verify score				09'0					0.51				_	-0.20				0.56			
Psi Blast		1.6e-86		1.6e-86					0.0000					9.6e-05		4.8e-54		4.8e-54			9.6e-09
END AA		367		366					268					280		370		367			349
STAR T AA		1		27					164					173		24		52			71
CHAI N ID		Ą		∢									-	A		A		Ą			
PDB ID		Iteh		Iteh					lvid				•	lybv	,	l ykt		1ykf			1a06
SEQ ID NO:		1838		1838					1838					1838	000	1838		1838			1839

	Γ						Г			_			Т																	_	_
PDB annotation	CALCIUM/CALMODULIN	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	KECEFIOR 2 SEKINE/THREONINE   KINASE	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMEKASE/FROIEIN KINASE),	KECEPTOR 2 SERINE/THREONINE   PUNIA SE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	PHOSPHOTRANSFERASE FGFR1K,	FIBROBLAST GROWTH FACTOR	RECEPTOR I; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP.	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFERASE
Coumpound	CHAIN: NULL;	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;			FK506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;			C-TERMINAL SRC KINASE;	CHAIN: A;		!	C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			FGF RECEPTOR 1; CHAIN: A, B;						
SEQFOL D score		58.79											62.45					_			_				70.22						
PMF score							90'0										0.00				10.0										
Verify score							-0.17										-0.33				-0.39										
Psi Blast		1.1e-15					1.5e-13						3.2e-27				1.5e-13				3.2e-27				1.1e-26						
END AA		350			_		199						337				197				334		-		339						
STAR T AA		50					70						73				78				87				64						
CHAI N ID		В					В			_			A				Ą				Ą				Ą						
PDB ID		1560					1b6c						Ibyg				1byg				1byg				lfgk						
SEQ ID NO:		1839					1839					,	1839				1839	_			1839				1839						

PDB annotation	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	COMPLEX (TRANSFERASE/SUBSTRATE)
Coumpound	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR 1; CHAIN: A, B;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN:
SEQFOL D score	71,37				61.82	
PMF score		0.41	0.10	0.33		0.16
Verify score		0,11	-0.20	-0.13		0.10
Psi Blast	3.2e-26	3.26-26	1.6e-27	1.4e-22	3.26-26	3.2e-26
END	338	335	332	321	350	332
STAR T AA	63	87	84	79	63	87
CHAI N ID	В	В	A		Y	A
PDB ID	lfgk	Ifgk	1fpu	1hcl	1ir3	lir3
SEQ ID NO:	1839	1839	1839	1839	1839	1839

PDB annotation	TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	TRANSFERASE KDR; TYROSINE KINASE	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
Coumpound	B;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TROPOMYOSIN; CHAIN: A, B, C, D	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	TRANSDUCIN; CHAIN; B, G; PHOSDUCIN; CHAIN: P;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score							
PMF score		0.29	0.03	-0.20	-0.13	-0.19	0.00
Verify score		-0.26	-0.38	0.14	0.19	0.53	-0.46
Psi Blast		1.1e-24	1.6e-20	8e-09	1.3e-08	4.5e-09	8e-23
END		347	336	176	164	112	191
STAR T AA		84	87	7	2	9	117
CHAI N ID		A	А	A	A	e4	A
PDB ID		1qcf	1vr2	lclg	Ireq	2trc	laih
SEQ ID NO:		1839	1839	1840	1840	1840	1841

PDB annotation		IINDING ZINC FINGER, DNA-BINDING PROTEIN				PROTEIN		COMPLEX (ZINC FINGER/DNA),		PROTEIN		,	INDING   ZINC FINGER, DNA-BINDING	PROTEIN				PROTEIN	_			PROTEIN	ULATION	NC NC	OES 102 -	ţ	ER		(ADRIB)	GOMPLEX (ZINC FINGER/DNA) ZINC		GER FINGER, PROTEIN-DNA
OL Coumpound	ė.	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	TRANSCRIPTION REGULATION	YEAST TRANSCRIPTION	FACTOR ADKI (RESIDUES 102 -	130) IAKD 3 (AMINO	TERMINAL ZINC FINGER	DOMAIN) (NMR, 10	STRUCTURES) IARD 4 (ADRIB)	DNA: CHAIN: A B D E		CONSENSOS ZINC FINGER
02	e D score		75.37									<u>.</u>																				
PMF	score						0.93				0.25				0.33				0.87				0.81							0.22	!	_
Verify	score						-0.18				90.0				-0.34				-0.66				-0.12							-0.12	!	
Psi Blast		,	6.4e-30				6.4e-30				3.2e-26				6.4e-24				6.4e-30				1.6e-06					_		1.6e-38		
END	AA		249				247				281				400				428				376							191	_	_
STAR	T AA		166				167				195				325				348				348							109		
CHAI	e N		A				Ą				Ą				Ą				٧						_		-			C		_
PDB	e		lalh				laih				lalh				lalh				lalh	•			lard							Imey	•	
SEQ	NO:		1841				1841				1841				1841				1841				1841							1841		_

PDB annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	INTERACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	NIEKACTION PROTEIN DESIGN 2
	(ZIV	S E	EZI ZI	CRY		(O)	Ĭ	Z	CRY	(215	COL	Z	C. S.		CO	Ĭ.	Z	CRY	(ZIP	CO	FIN	Z	CRY	(Z)	CO	Ž	E	CR		CON	Ž	Z
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	PROTEIN CHAIN F G			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN: CHAIN: C. F. G.
SEQFOL D score											83.84																					
PMF score		0.98				1.00									0.22					0.22					0.82					0.70		
Verify score		-0.01				0.11					-				-0.14					-0.60					-0.19			·		0.13		
Psi Blast		1.6e-47		-		1.6e-48					1.6e-48				8e-45					1,1e-41					1.6e-45					1.1e-12		
END		219				247					248				282					400					428					247		_
STAR T AA		138				166					166				194					324					347					220		
CHAI N ID		ပ				ပ					ပ				၁					၁					ပ					Ü		
PDB ID		1mey				1mey					Imey				1mey			_		lmey					1mey	<del>-</del>				1mey		-
SEQ ID NO:		1841			,	1841					1841				1841					1841			_		1841			•		1841		_

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation	
NO:	III	ar N	I AA	AA		score	score	D score			
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER)DNA)	
1841	lmey	g	345	372	6.4e-13	-0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSIS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN-DNA	,
				-					PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2	
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	
1841	1mey	G	401	428	1.6e-13	0.03	0.48		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC	
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA	
									FROTEIN; CHAIN: C, F, G;	CRYSTAI STRICTIRE COMPLEX	
										(ZINC FINGER/DNA)	
1841	1sp2		348	376	8e-09	-0.21	0.03		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION	
										FACTOR SP1; ZINC FINGER,	
711	1+63		105	200	1 1 00	200	-		ATT GOTTO ATT MONTHER BY	IKANSCKIPTION ACTIVATION, SPI	
1841	CIII	Ą	561	/07	1.1e-20	0.03	-0.11		IRANSCRIPTION FACTOR IIIA;	COMPLEX (TRANSCRIPTION	
	· · · · ·								CHAIN: A; 3S KNA GENE; CHAIN: F F:	REGULATION/DNA) IFIIIA; 58 GENE: NMR TEITA PROTEIN DNA	
	_									TRANSCRIPTION FACTOR, 58 RNA 2	
			-							GENE, DNA BINDING PROTEIN,	
										ZINC FINGER, COMPLEX 3	
										(TRANSCRIPTION	
,	,									REGULATION/DNA)	
1841	Itf6	Ą	112	278	3.2e-33			74.20	TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION	
									KIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX	
<del></del> -	_					_	_		CHAIN: B, C, E, F;	(TRANSCRIPTION	
			•							REGULATION/DNA), RNA	
			•							POLYMERASE III, 2	
						10.0				TRANSCRIPTION INITIATION, ZINC	
1										FINGER PROTEIN	
1841	1tf6	¥	139	284	3.2e-33	-0.25	0.49		TFIIIA; CHAIN: A, D; 5S DIBOSOMAI DNA GENE:	COMPLEX (TRANSCRIPTION DEGIT ATTOMICAL COMPLEY	
			_	• • • • • •					CHAIN: B C B F.	(TRANSCRIPTION	
										REGULATION/DNA), RNA	

M I	PDB CHAI	AI STAR D TAA	R END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
1									POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1tf6	9 Y	297	437	4.8e-31	-0.30	0.19		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
	· <del></del>							CHAIN: B, C, E, F;	(TRANSCRIPTION ) REGULATION/DNA). RNA
									POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC
15	+		-						FINGER PROTEIN
1 <u>±</u> 2	, 9	348	488	6.4e-34	-0.37	0.04		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
		<del>- ··</del> ····						CHAIN: B, C, E, F;	(TRANSCRIPTION REGULATION/DNA), RNA
									POLYMERASE III, 2
									TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1ubd	pq C	601	219	3.2e-30	-0.16	0.19		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
	_							ASSOCIATED VIKUS PS INITIATOR ELEMENT DNA;	REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION.
								CHAIN: A, B;	INITIATOR ELEMENT, YY1, ZINC 2
		_							FINGER PROTEIN, DNA-PROTEIN  PECOCNITION 2 COMPLEY
									CTR ANSCRIPTION
									REGULATION/DNA)
1ubd	pq C	140	248	3e-32			77.97	YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION
								ASSOCIATED VIRUS P5	REGULATION/DNA) YING-YANG 1;
							•	INITIATOR ELEMENT DNA;	TRANSCRIPTION INITIATION,
								CHAIN: A, B;	INITIATOR ELEMENT, YYL, ZINCZ FINGER PROTEIN DNA-PROTFIN
									RECOGNITION, 3 COMPLEX
									(TRANSCRIPTION
[	2	142	247	2, 22	,,,,	0.70		VIVITA D. TATA D. C. APPATO	REGULATION/DNA)
Ingg	$\dashv$	143	1.247	3e-32	-0.33	0.78		YYI; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

und PDB annotation	US P5  REGULATION/DNA) YING-YANG 1;  SNT DNA;  INTIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)		NA;	CRIPTION A) TEIN (TWO RIDE) H 2DRP 3	TEIN GLII; COMPLEX (DNA-BINDING HAIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GII ZING FINGED COMPI EV CONA
OL Coumpound	ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score					76.50
PMF score		0.04	0.40	0.01	
Verify score		-0.25	-0.46	-0.52	
Psi Blast		3.2e-32	6.4e-30	4.8e-06	1.6e-32
END		281	428	371	283
STAR T AA		174	332	323	138
CHAI N ID		ပ	O	A	A
PDB ID		lubd	lubd	2drp	2gli
SEQ NO.		1841	1841	1841	1841

			 														_							
PDB annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA HEI ICAL LINKER REGION 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEA, MULII-SUBUMII	NSECI-PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	NSECI; PROTEIN-PROTEIN	COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX
Coumpound	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	ALPHA SPECTRIN; CHAIN; A, B, C;			ALPHA SPECTRIN; CHAIN: A,	B, C;			SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CYNITA YRI BINIDING DROTTER!	1: CHAIN: A: SYNTAXIN 1A:	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C;				SYNTAXIN-1A; CHAIN: A, B, C;		
SEQFOL D score				,																				
PMF score		-0.05	-0.17			0.00				-0.20		000	07:0-		-0.17			-0.19				-0.19		
Verify score		0.09	1.09			0.39				0.41		0 57	70.0		0.43			0.78				0.83		
Psi Blast		1.6e-32	1.5e-09			7.5e-05				4.5e-10		1 50.17	1.20.1		1.5e-11			1e-09				3e-16		
END AA		283	648			862				613		6/12	7		769			576				601		
STAR T AA		146	511			566				437		481	Ď		513			447				485		
CHAI N ID		A	∀			A				В		ď	٦		В			∀				A		
PDB ID		2gli	Icun			Icun				1dn1		1dh1			ldnl			lez3	•			lez3		
SEQ ID NO:		1841	1845			1845				1845		1845	} 		1845			1845				1845		

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ÿ	a a	9 Z	TAA	AA		score	score	D score		
										BUNDLE
1845	lez3	A	511	920	1.5e-16	1.11	-0.20		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS
										SYNAPTOTAGMIN ASSOCIATED 35
										KDA PROTEIN, P35A, THREE HELIX
										BUNDLE
1845	1ez3	Ą	526	859	3e-16	86.0	-0.17		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS
										SYNAPTOTAGMIN ASSOCIATED 35
								-		KDA PROTEIN, P35A, THREE HELIX
										BUNDLE
1845	lez3	Ą	739	861	4.5e-05	0.21	0.00		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS
										SYNAPTOTAGMIN ASSOCIATED 35
										KDA PROTEIN, P35A, THREE HELIX
										BUNDLE
1845	1f5n	٧	485	979	3e <b>-</b> 08	0.74	-0.19		INTERFERON-INDUCED	SIGNALING PROTEIN GBP, GTP
								.,	GUANYLATE-BINDING	HYDROLYSIS, GDP, GMP,
									PROTEIN 1; CHAIN: A;	INTERFERON INDUCED, DYNAMIN
										2 RELATED, LARGE GTPASE
										FAMILY, GMPPNP, GPPNHP.
1845	lfio	∢	485	642	9e-13	0.55	-0.20		SSO1 PROTEIN; CHAIN: A;	MEMBRANE PROTEIN FOUR HELIX
										BUNDLE, ALPHA HELIX
1845	1dnn	Ą	460	959	3e-24	0.70	-0.19		HUMAN SKELETAL MUSCLE	CONTRACTILE PROTEIN TRIPLE-
									ALPHA-ACTININ 2; CHAIN: A;	HELIX COILED COIL,
										CONTRACTILE PROTEIN
1845	lred	Ą	451	746	4.5e-31	0.48	-0.08		METHYLMALONYL-COA	ISOMERASE ISOMERASE, MUTASE,
									MUTASE; CHAIN: A, B, C, D;	INTRAMOLECULAR TRANSFERASE
1845	Isig		485	643	4.5e-18	0.76	-0.15		RNA POLYMERASE PRIMARY	TRANSCRIPTION REGULATION
									SIGMA FACTOR; CHAIN: NULL;	SIGMA70; RNA POLYMERASE
										SIGMA FACTOR, TRANSCRIPTION
										REGULATION
1845	Isig		486	229	6e-17	0.40	-0.20		RNA POLYMERASE PRIMARY	TRANSCRIPTION REGULATION
-									SIGMA FACTOR; CHAIN: NULL;	SIGMA70; RNA POLYMERASE
										SIGMA FACTOR, TRANSCRIPTION
1915	24.00		100	601	1 50 17				C a latito racitabili an	KEGULATION
10+01	2117	4	400	021	1.36-17	0.22	-0.20		IKANSDUCIN; CHAIN: B, G;	COMPLEX

PDB annotation	(TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCIN, BETA-BAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
Coumpound	PHOSDUCIN; CHAIN: P;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;
SEQFOL D score				
PMF score		-0.19	-0.20	0.59
Verify score		0.29	0.23	-0.68
Psi Blast		1.5e-20	1.5e-13	1.1e-07
END AA		647	746	55
STAR T AA		513	577	29
CHAI N ID	7	۵۰	Д.	
PDB ID		2trc	2trc	1bor
SEQ ID NO:		1845	1845	1849

PDB annotation	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP- 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP- 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP- 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP-2 120	TRANSFERASE
Coumpound	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: A, B;                                                                                                 GLYCINE N-				
SEQFOL D score	64.85			62.06				
PMF score		66.0	1.00	•	0.95	0.96	66.0	0.21
Verify score		0.47	0.54		0.11	0.52	0.52	-0.00
Psi Blast	4.5e-30	4.5e-30	1.3e-19	6e-36	1.6e-13	1,3e-19	6e-36	7.5e-06
END AA	200	498	499	515	494	528	528	331
STAR T AA	397	398	398	306	359	395	397	175
CHAI N ID				<b>V</b>	A	A	A	A
PDB TD	lksr	1ksr	1ksr	1qfh	1qfh	1qfh	1qfh	1d2h
SEQ ID NO:	1849	1849	1849	1849	1849	1849	1849	1850

		II	Ü ÆR	K,		IA; JING, 1AIN,	IA;
ion	3	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GARPBETA 1: COMPI FX
PDB annotation	METHYL TRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN METHANOCOCCUS JANNA	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIX ALPHA-BETA, HEXAMER, 2 DI	NE CEL NE, REP		COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPAL GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BI REGULATION/DNA), DNA-BI 2 NUCLEAR PROTEIN, ETS DANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPAI GABPBETA1: COMPI EX
PDE	7LTRAN	TURAL	FERASE IN, BETA -BETA,	NCOGE NCOGE T		COMPLEX (TRANSC REGULATION/DNA) GABPBETA1; COMPI (TRANSCRIPTION REGULATION/DNA), 2 NUCLEAR PROTEII ANKYRIN REPEATS,	COMPLEX (TRANSCRIP REGULATION/DNA) GAI GABPBETA1: COMPLEX
	METHY	STRUC HYPOI METHA	TRANS DOMA ALPHA	ANTI-ON ANTI-ON REPEAT		COMPI REGUI GABPB (TRAN) REGUI 2 NUCI ANKYF	COMPI REGUL GABPB
					DTRA INASE APM 3 ALPHA ITH ED BY C WITH	LPHA; i: B;	LPHA; [: B;
puno	FERASE );	.;	IE N- FERASE 5, 6;	SSOR N: NULL	PHOSPH AMP\$- DTEIN K 'APK\$) 1 BUNIT) TANT W REPLAC OMPLEY PM 5 F-24) AN GA-8 1A	OTEIN A NDING .; CHAIN B;	OTEIN A NDING CHAIR
Coumpound	TRANSI A, B, C, I	CHAIN:	ARGININ TRANSI , 2, 3, 4,	SUPPRE A; CHAI	SEASE(F) SE) \$C-// ENT PR( .37) (\$C/ /TIC SU ME MU 1APM 4 1 139A\$) C TIDE 1A	A; GA BI BETA 1 AIN: D,	ING PRO I, GA BI I BETA 1
	METHYLTRANSFERASE; CHAIN: A, B, C, D;	MJ0882; CHAIN: A;	HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TUMOR SUPPRESSOR PIGINK4A; CHAIN: NULL;	TRANSFERASE(PHOSPHOTRA NSFERASE) \$C-/AMP\$- DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (\$C/APK\$) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B:
SEQFOL D score					99.80		
					66		
PMF	<u></u>	0.01	0.04	 0.95		1.00	1.00
Verify score		0.24	0.11	0.39		0.33	0.55
Psi Blast		6.4e-09	1.3e-14	4.5e-32	4.5e-30	.5e-36	7.5e-43
<u> </u>							
END		294	292	899	349	604	637
STAR T AA		177	148	538	_	447	486
CHAI N ID		A	-		កា	æ	В
PDB ID		1dus	1 <u>g</u> 6q	1a5e	lapm	lawc	Iawc
SEQ ID NO:		1850	1850	1853	1853	1853	1853

CE	CHAI N D	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
								DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
В		551	705	1.26-45			94.92	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
В		556	704	6.4e-35	0.72	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
м ,		584	737	1.2e-45	0.70	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
Ф		617	770	1.5e-44	0.60	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,

PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGIT ATTON/DNA) GARPAL PHA:	GABPBETA1; COMPLEX	(TRAINSCRIFTION) REGULATION/DNA), DNA-BINDING.	2 NUCLEAR PROTEÍN, ETS DOMAIN,	ANKYKIN KEPEAIS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETAL; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING.	2 NUCLEAR PROTEÍN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION) GABPALPHA:	GABPBETA1; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (ISOMERASE/PROTEIN	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE KINASE
Coumpound	2 N AN TR	GA BINDING PROTEIN ALPHA; CO	CHAIN: B;	DIVA; CHAIN: D, E; (TR	N 2	AN	ALPHA;		PROTEIN BETA I; CHAIN: B; GA DNA: CHAIN: D. E:		2N	AN	$\dashv$	GA BINDING PROTEIN ALPHA; COI	Ä. Ä.		RE	2 N	AN		FK506-BINDING PROTEIN; CHAIN: A C F G: TGF.B				RE
SEQFOL D score															•	•		•					•		
PMF		1.00					1.00							1.00						,	1.00				
Verify score		0.63					0.34							0.74						Į.	0.37				•
Psi Blast		1.5e-42					1.6e-32							3e-35							3e-49				
END		802					802							828						ì	276				
STAR T AA		651					929							289							97				
CHAI N ID		В					В					-		B				-		6	2				
PDB ID		lawc					1awc							lawc						11	1000				
SEQ ID NO:		1853			-		1853							1853						1050	1853				

PDB annotation		TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDR4/0 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF				KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	—			KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)			KINASE CELI CYCLE CONTROL
Coumpound		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR;	CHAIN: NOLL;	P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		P19INK4D CDK4/6 INHIBITOR;	CHAIN: NULL;		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; PIYINK4D; CHAIN:	ģ;
SEQFOL	D score																													
PMF	score	0,49	1.00		1.00		1.00			1.00			1.00			1.00						1.00						1.00		
Verify	score	0.37	99.0		0.58		0.76			0.32			0.51			0.21						0.77						0.63		
Psi Blast		4.8e-10	4.5e-35		1.4e-40		1.5e-44			6e-42			1.5e-40			1.1e-36				-		3e-43						1.5e-41		
END	AA	574	909		637		673			739			805			019						673						743		
STAR	T WW	445	458		486		518			585			652			447						521						587		
CHAI																В						В						В		
PDB	=	1bd8	1bd8		1bd8		1bd8		:	lbd8			1bd8			lblx						lblx						1blx	_	
SEQ	NO:	1853	1853		1853		1853		1	1853			1853			1853						1853						1853		

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
NO:	a	UN III	I AA	AA		score	score	D score		
										ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1blx	В	651	808	4.5e-41	09.0	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
										KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1853	1bu9	¥	444	576	8e-09	0.16	0.87		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INHIBITOR,
										P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1bu9	А	486	612	4.5e-33	09.0	1.00		CYCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-
									o infilbi i OK; Chain; A;	INNAC; CELL CICLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR,
										CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1853	1byg	А	24	276	1.4e-45	0.81	96.0		C-TERMINAL SRC KINASE;	TRANSFERASE CSK; PROTEIN
									CHAIN: A;	KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1057	-	F	-	9	000				my range resulting Care	STAUROSPORINE, TRANSFERASE
1833	ıcınk	ъ	-	349	1.5e-30			96.05	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN	
					-				KINASE CATALYTIC SUBUNIT	
									1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1853	1ctp	田		342	1.5e-30			92.53	TRANSFERASE(PHOSPHOTRA	
									NSFERASE) CAMP-	
									DEPENDENT PROTEIN KINASE	
									(E.C.Z./.1.3/) (CAFK) 1C1F 3 (CATALYTIC SUBUNIT) 1CTP 4	
1853	1d9s	А	478	610	1e-35	0.73	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-
									4 INHIBITOR B; CHAIN: A;	HELIX, ANKYRIN REPEAT
1853	1d9s	А	510	637	1.5e-33	0.36	1.00		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN-

PDB annotation	: A; HELIX, ANKYRIN REPEAT	KINASE SIGNALING PROTEIN HELIX-TURN- EA; A; HELIX, ANKYRIN REPEAT			ASE			BINDING MODULE, ANKYRIN REPEATS, METAL BINDING	PROTEIN		FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	·   RECEPTOR,	PHOSPHOTRANSFERASE		FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFERASE	IN: A, B; PHOSPHOTRANSFERASE FGFRIK,	FIBNOBLAST ONOW HITFACTOR	MECEFIUNI; INANSFERASE,	1 YROSINE-PROTEIN KINASE, ATP-	BECEPTOR	TATOONIO AGENTALIA
Coumpound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;		FGF RECEPTOR 1; CHAIN: A, B;				-			FGF RECEPTOR 1; CHAIN: A, B;							FGF RECEPTOR 1; CHAIN: A, B;					
SEQFOL D score									:	114.87														112.87				_	
PMF score		1.00	1.00	1.00	0.92		0.51										1.00												
Verify score		0.65	0.36	0.43	0.54		0.13										0.46												
Psi Blast		7.5e-38	9e-37	1.2e-34	36-34		4.5e-32			1.5e-45							1.5e-45							7.5e-45					
END AA		673	743	773	807		694			293							276							292					
STAR T AA		545	809	645	677		513			18							26							_					
CHAI N ID		Ą	Ą	A	A		Ą			A							¥							В					
PDB ID		1d9s	1d9s	1d9s	1d9s		1dcq			1fgk							1fgk							Ifgk					·
SEQ NO.		1853	1853	1853	1853		1853			1853							1853							1853					

PDB CHAI STAR END P	STAR END	END		4	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
N ID 1 AA	1 AA		AA			score	score	D score		
1fgk B 26 276 7.5e-45 0.50	26 276 7.56-45	276 7.5e-45	7.5e-45		0.	0	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GROWTH FACTOR
										RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-
										BINDING, 2 PHOSPHORYLATION,
										RECEPTOR, PHOSPHOTRANSFERASE
1fmk 26 276 1.2e-46 0.79	276 1.2e-46	276 1.2e-46	1.2e-46	46	0.79		1.00		TYROSINE-PROTEIN KINASE	PHOSPHOTRANSFERASE C-SRC,
									SRC; CHAIN: NULL;	P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2
										PHOSPHOTYROSINE, PROTO-
										ONCOGENE,
1fpu A 49 276 7.5e-45 0.51	49 276 7.5e-45	276 7.5e-45	7.5e-45	45	0.51		1.00		PROTO-ONCOGENE	TRANSFERASE P150, C-ABL;
									TYROSINE-PROTEIN KINASE	KINASE, KINASE INHIBITOR, STI-
			1						ABL; CHAIN: A, B;	571, ACTIVATION LOOP
Ihcl	326	326		9e-28				92.94	HUMAN CYCLIN-DEPENDENT	PROTEIN KINASE CDK2;
									KINASE 2; CHAIN: NULL;	TRANSFERASE,
										SERINE/THREONINE PROTEIN
										KINASE, ATP-BINDING, 2 CELL
				<del></del>						CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYT.ATION
lihb A 484 608 3e-34 0.36	484 608 3e-34	608 3e-34	3e-34		0.36		1.00		CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-
									6 INHIBITOR; CHAIN: A, B;	INK4C(INK6); CELL CYCLE
										INHIBITOR, P18-INK4C(INK6),
										ANKYRIN REPEAT, 2 CDK 4/6
1ikn D 458 647 4 5e-46 0.41	458 647 4 5e-46	647 4 56-46	4 5e-46	46	0.41		1 00		NF.K APPA.B P65 SUBUNIT.	TRANSCRIPTION FACTOR P65:
	01-01-1	200	0t-00:t	<u> </u>			00:1		CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN; C: I-KAPPA-	IKB/NFKB COMPLEX
									B-ALPHA; CHAIN: D;	
likn D 486 680 6e-53 0.41	486   680   6e-53	680 6e-53	6e-53		0.4		1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
				<del></del> -					CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
									SUBUNIT; CHAIN: C; I-KAPPA-	IKB/NFKB COMPLEX

							_			_																								L	
PDB annotation			TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TO A CHO A TI COMMITTED DICA CIT.	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		COMPLEX	(TRANSFERASE/SUBSTRATE)	TYROSINE KINASE, SIGNAL	TRANSDUCTION,	PHOSPHOTRANSFERASE, 2	COMPLEX (KINASE/PEPTIDE	SUBSTRATE/ATP ANALOG),	ENZYME, 3 COMPLEX	(TRANSFERASE/SUBSTRATE)	COMPLEX	(TRANSFERASE/SUBSTRATE)	TYROSINE KINASE, SIGNAL	TRANSDUCTION,	PHOSPHOTRANSFERASE, 2	COMPLEX (KINASE/PEPTIDE	SUBSTRATE/ATP ANALOG),	ENZYME, 3 COMPLEX	(TRANSFERASE/SUBSTRATE)	ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	ANIX DEBEATANCED CONTING
Coumpound		B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-BA-BA-BA-BA-BA-BA-BA-BA-BA-BA-BA-BA-BA	ME VADDA DING CIMITALITY	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	INSULIN RECEPTOR; CHAIN: A;	PEPTIDE SUBSTRATE; CHAIN:	B;							INSULIN RECEPTOR; CHAIN: A;	PEPTIDE SUBSTRATE; CHAIN:	B;							MYOTROPHIN; CHAIN: NULL		MVOTPOPHINI CHAINI NI I
SEQFOL D score	31035														114.32																				
PMF	2020		1.00			1 00	00.1				1.00													1.00									0.93		00
Verify			0.21			20.0	97.0				0.15											••		0.65									0.46		0.46
Psi Blast			6e-58			1 50 50	4.3e-3Z				1.3e-54				1.5e-46	•							-	1.5e-46					_				8e-13		9e-23
END			749			775	C//				810				306									276									523		563
STAR			551			504	284				617				10	_								26									445		458
CHAI			Q			6	ב				Д				A			_						∀											
PDB ID			likn			1.1/2					1ikn			$\dashv$	lir3									lir3				-					lmyo		lmyo
SEQ ID	NO:		1853			1853	. ccol				1853				1853									1853									1853		1853

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
e ë	A	OI N	TAA	AA		score	score	D score		
										ACETYLATION, NMR, ANK-REPEAT
1853	1myo		461	685	<b>8e-</b> 16	90.0-	0.46		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1853	1myo		521	635	4.5e-32	0.55	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYL ATION NMR ANK-REPEAT
1853	1myo		554	699	1.5e-36	0.44	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
										ACETYLATION, NMR, ANK-REPEAT
1853	lmyo		621	735	1.5e-32	0.34	0.99		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYI ATION NAMP ANK-PEPEAT
1853	1myo		654	768	3e-33	-0.03	0.57		MYOTROPHIN: CHAIN: NULL	ANK-REPEAT MYOTROPHIN.
	•					_				ACETYLATION, NMR, ANK-REPEAT
1853	1myo		684	800	1.5e-30	0.37	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
										ACETYLATION, NMR, ANK-REPEAT
1853	Infi	ш	461	637	6e-43	0.50	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
	-								I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									F;	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1853	Infi	m	484	229	3e-50	0.52	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
									NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									ŗŗ,	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1853	lnfi	ш	549	749	1.2e-53	0.54	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
	•								NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
									F;	REGULATION/ANK REPEAT),
										ANKYRIN 2 REPEAT HELIX
1853	Infi	ப	581	778	1.5e-53	0.20	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION
				_		_			NF-KAPPA-B P50; CHAIN: B, D;	REG/ANK REPEAT) COMPLEX
									I-KAPPA-B-ALPHA; CHAIN: E,	(TRANSCRIPTION
	-								ŗ.	REGULATION/ANK REPEAT),
1	,	!								ANKYRIN 2 REPEAT HELIX
1853	Infi	Э	919	815	1.5e-53	0.56	1.00		NF-KAPPA-B P65; CHAIN: A, C;	COMPLEX (TRANSCRIPTION

PDB annotation		REG/ANK REPEAT) COMPLEX (TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYKIN 2 KEPEAT HELLX	TRANSFERASE MITOGEN	ACTIVATED PROTEIN KINASE;	TRANSFERASE, MAP KINASE,	SERINE/THREONINE-PROTEIN	KINASE, 2 P38	IKANSFEKASE MAP KINASE,	SEKINE/IHKEONINE PROTEIN	KINASE, IKANSFEKASE	TYROSINE KINASE TYROSINE	KINASE-INHIBITOR COMPLEX,	DOWN-REGULATED KINASE, 2	ORDERED ACTIVATION LOOP	TRANSFERASE ALPHA BETA FOLD	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ANKYRIN REPEATS, CELL-CYCLE	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ANKYRIN REPEATS, CELL-CYCLE	COMPLEX (ANTI-	ONCOGENE/ANKYRIN REPEATS)	P53BP2; ANK YRIN REPEATS, SH3,	P53, TUMOR SUPPRESSOR,	MULTIGENE 2 FAMILY, NUCLEAR	PROTEIN, PHOSPHORYLATION,	DISEASE MUTATION, 3	POLYMORPHISM, COMPLEX (ANTI-	ONCOGENE/ANKYKIN KEPEAIS)	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound		NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E,	Ė		MAP KINASE P38; CHAIN:	NULL;				EKKZ; CHAIN: NOLL;			HAEMATOPOETIC CELL	KINASE (HCK); CHAIN: A;		:	LCK KINASE; CHAIN: A;	REGULATORY PROTEIN SWI6;	CHAIN: A, B;	!	REGULATORY PROTEIN SWI6;	CHAIN: A, B;		P53; CHAIN: A; 53BP2; CHAIN:									P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL	D score			1,	92.67					97.49																							
PMF	score												1.00		-		1.00	0.10			00.0			96'0							·		1.00
Verify	score												99.0				0.71	-0.40			-0.17			0.27									0.31
Psi Blast					3e-27				0	oe-73		,	1.5e-49				7.5e-50	1.5e-17			1.5e-40			3.2e-12		•							6.4e-12
END	AA			0.00	359				0	228		1	276			,	276	592			652			503									578
STAR	I AA				বা				ì,	<u>c</u>		ļ	56				26	466			512			452								(	458
CHAI	N ID												¥				Ą	Ą			Ą			В									<b>a</b>
PDB	a				1p38				,	1pme		,	Idet				1qpc	1sw6			1sw6			1ycs									lycs
SEQ	NO:			0	1853				0,0	1833			1853				1853	1853			1853			1853								0	1853

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PDB annotation	P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
Coumpound		P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;	P53; CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score				
PMF score		0.99	66.0	0.30
Verify score		60.00	0.26	-0.13
Psi Blast		6e-33	1.4e-38	7.5e-33
END		099	726	608
STAR T AA		488	554	654
CHAI N ID		m	В	Д
PDB ID		1ycs	lycs	1ycs
SEQ ID NO:		1853	1853	1853

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PDB annotation	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
Coumpound	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	RAB6 GTPASE; CHAIN: A;	RAS-RELATED C3 BOTUL.NUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;
SEQFOL D score	107.86	85.26			77.02		
PMF score			1.00	1.00		1.00	0.59
Verify score			0.43	0.55		0.48	0.12
Psi Blast	9e-31	9.6e-68	9.66-68	1.6e-68	1.6e-68	6.4e-56	3.2e-53
END AA	356	171	173	173	174	171	176
STAR T AA	۶		1	<b></b>	1	3	-
CHAI N ID		Ą	Ą	Ą	Ą	А	A
PDB ID	3erk	lcly	lcly	lctq	lctq	1d5c	1486
SEQ ID NO:	1853	1854	1854	1854	1854	1854	1854

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY		COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-
Coumpound	GTP-BINDING PROTEIN YPT51; CHAIN: A;	RAP2A; CHAIN: NULL;	RAP2A; CHAIN: NULL;	RAC1; CHAIN: NULL;	RAC1; CHAIN: NULL;	ONCOGENE PROTEIN C-H-RAS P21 PROTEIN MUTANT WITH GLY 12 REPLACED BY PRO IPLJ 3 (G12P) COMPLEXED WITH P3-1-(2- NITROPHENYL)ETHYL- IPLJ 4 GUANOSINE-5'-(B,G-IMIDO)- TRIPHOSPHATE IPLJ 5	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	RAB-3A; CHĀIN: A; RABPHILIN-3A; CHAIN: B;
SEQFOL D score			95.27	52.65			50.36	60.15
PMF score	1.00	1.00			0.94	1.00		
Verify score	0.31	0.49			0.28	0.37		
Psi Blast	6.4e-55	4.8e-64	4.8e-64	1.1e-53	1.1e-53	4.8c-52	4.8e-36	8e-59
END	174	171	174	174	176	171	186	179
STAR T AA	П	1	-		2	1	2	1
CHAI N ID	A						O	A
PDB ID	1ek0	1kao	1kao	1mh1	1mh1	iplj I	dri)	1zbd
SEQ ID NO:	1854	1854	1854	1854	1854	1854	1854	1854

PDB annotation	BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN		HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROL YSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	FIN; COMPLEX (SERINE PROTEASE/INHIBITOR) SKIN-DERIVED ANTILEUKOPROTEINASE (SKALP); HYDROLASE, SERINE PROTEASE, 3D-STRUCTURE, ZYMOGEN, PANCREAS, 2 SIGNAL, COMPLEX (SERINE PROTEASE/INHIBITOR)
Coumpound		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A: GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B:	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;	ELASTASE; CHAIN: E; ELAFIN; CHAIN: I;
SEQFOL D score			54.33	68.59		
PMF score		96'0			0.99	0.48
Verify		0.43			0.27	-0.71
Psi Blast		8e-59	3.2e-50	1.1e-59	1.1e-59	3.2e-16
END AA		176	193	174	174	72
STAR T AA		4	-	2	4	29
CHAI N ID		V	A	A	A	
PDB ID		1zbd	2ngr	3rab	3rab	1fle
SEQ ID NO:		1854	1854	1854	1854	1856

PDB annotation	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R- ELAFIN, ELASTASE INHIBITOR	SICNAT ING DB OTEN CTB BINDING	PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS		SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX,	ENDOCYTOSIS/EXOCYTOSIS G-	PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	G PROTEIN G PROTEIN, RAS, ARF, ARF, ARF6, MEMBRANE TRAFFIC	ENDOCYTOSIS/EXOCYTOSIS G	PROTEIN, VESICULAR TRAFFIC,	GTP HYDROLYSIS, YPT/RAB 2	FROTEIN, ENDOCTIOSIS, HYDROLASE	SIGNALING PROTEIN ARF-LIKE	PROTEIN 3, ARL3; PROTEIN-GDP	COMPLEX WITHOUT MAGNESIUM,	G-DOMAIN	PROTEIN TRANSPORT GDP-	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16	PROTEIN TRANSPORT GDP-
Coumpound	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	R-ELAFIN; CHAIN: NULL;	DAS DEI ATEN BAB	1A; CHAIN: A; PROTO- ONKOGENE	SERINE/THREONINE PROTEIN KINASE CHAIN: B;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN:	RAB6 GTPASE; CHAIN: A;		ADP-RIBOSYLATION FACTOR 6: CHAIN: A:	GTP-BINDING PROTEIN YPT51;	CHAIN: A;			ADP-RIBOSYLATION FACTOR-	LIKE PROTEIN 3; CHAIN: A;			HUMAN ADP-RIBOSYLATION	FACTOR 1; 1HUR 5 CHAIN: A, B; 1HUR 7	HUMAN ADP-RIBOSYLATION
SEQFOL D score			50.43	C+:0C														83.99		
PMF score	0.12	0.46				0.01	0.01		1.00	-0.13				1.00						0.92
Verify score	-0.54	-0.02				-0.14	-0.22		0.11	90.0				0.50						0.23
Psi Blast	0.0011	1.6e-17	50.090	7.00		1.6e-28	3.2e-30		4.8e-52	3.2e-28				1.1e-48				6.4e-57		6.4e-57
END	80	72	177			185	183		191	183				190				182		192
STAR T AA	32	20	101	7		23	21		14	22	4,41			7				9		9
CHAI N ID	A			ζ.		A	A		A	A				A				А		A
PDB ID	ligr	2rel	1013	)		1cxz	1d5c		1e0s	1ek0				1fzq				1hur		1hur.
SEQ ID NO:	1856	1856	1857	, CB 1		1857	1857		1857	1857				1857				1857		1857

PDB annotation	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE),	GIFASE, 2 IKANSIIION SIAIE, GAF	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP	HYDROLYSIS, RAB 2 PROTEIN,	NEUKU I KANSMII I EK KELEASE, HYDROLASE	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING	PROIEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Coumpound	FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	RAP2A; CHAIN: NULL;	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	161110	KAB3A; CHAIN: A;			QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SILE; CHAIN; B, C;	OGSK ZINC FINGER PEPTIDE;	OLIGONICLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING STEF: CHAIN: B. C.	DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	
SEQFOL D score		50.54								000	58.29									
PMF score			-0.03	0	0.30			0.28						0.51			0.09			
Verify score			0.22	200	-0.03			-0.07						0.40			-0.22			
Psi Blast		1.6e-24	1.6e-27	000	5.26-33	, ,		3.2e-30		20.01	3.2e-31	,		3.2e-31			3.2e-50			
END		186	185	5	<u> </u>			132		1/2	791			160			188			
STAR T AA		19	23	5	77			52		7,6	9/			80			107			
CHAI N ID			В		₹			A			٧			Ą			C			
PDB ID		1kao	1tx4	197	3ra0			lalh		1015	lain			la1h		_	1mey			
SEQ ID NO:		1857	1857	1057	1637			1858		1050	1638			1858		_	1858			

		1	I		r	
PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
Соимроии	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, B; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 58 RNA GENE; CHAIN: E, F;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score			62.32			
PMF score	0.17	86.0		0.24	0.39	0.10
Verify score	-0.18	0.17		0.14	-0.08	-0.10
Psi Blast	4.8e-50	1.4e-50	1,4e-50	3.2e-20	1.3e-34	3.2e-33
END	132	160	161	160	160	162
STAR T AA	51	79	79	08	56	11
CHAI N ID	O	၁	C	A	O	4
PDB ID	Imey	1mey	lmey	143	1ubd	2gli
SEQ ID NO:	1858	1858	1858	1858	1858	1858

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										BINDING PROTEIN/DNA)
1858	2gli	Ą	51	188	4.8e-34			58.21	ZINC FINGER PROTEIN GL11; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1858	2gli	A	59	188	4.8e-34	-0.37	0.11		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1859	la1h	⋖	115	198	6.4e-29			60.10	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	lalh	A	117	197	6.4e-29	-0.04	0.78		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
									OLIGONUCLEUTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
1859	laih	∢	145	237	4.8e-27	-0.23	0.35		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	la1h	А	212	273	6.4e-15	0.07	-0.13		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	la1h	Ą	96	169	3.2e-25	-0.26	0.10		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1859	Imey	ပ	116	197	1.6e-50	-0,03	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ NO	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										(ZINC FINGER/DNA)
1859	1mey	၁	116	198	1.6e-50			70.79	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
				-						CRYSTAL STRUCTURE, COMPLEX
1859	lmey	C	144	237	1.3e-46	-0.02	0.43		DNA: CHAIN: A. B. D. E:	COMPLEX (ZINC FINGER/DNA) ZINC
							!		CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CKISIAL SIKUCIUKE, CUMPLEA (ZINC FINGER/DNA)
1859	lmey	၁	172	265	1.1e-33	-0.35	0.12		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN DNA
									PROTEIN: CHAIN: C. F. G:	INTERACTION PROTEIN DESIGN 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1859	Imey	ပ	85	141	1.4e-26	-0.22	0.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
					_					CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1859	lmey	ပ	88	169	1.1e-41	-0.10	0.35		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
0.0		ļ		-	;					(ZINC FINGEKUDNA)
1859	Imey	ڻ	209	237	1.4e-11	-0.11	0.42		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
	_									CRYSIAL SIRUCIUKE, COMPLEX
	J,			1	,					(ZINC FINGER/DINA)
1859	Ipaa		212	239	8e-06	-0.29	0.81		TRANSCRIPTION REGULATION	
_									YEAST TRANSCRIPTION	
									FACTOR ADRI (RESIDUES 130 -	- Marian and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second

PDB annotation		ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION
Coumpound	159) IPAA 3 (PAPA - CARBOXY TERMINAL ZINC FINGER DOMAIN) MUTANT WITH IPAA 4 PRO 131 REPLACED BY ALA, PRO 133 REPLACED BY ALA, CYS 140 IPAA 5 REPLACED BY ALA (P131A,P133A,C140A) (NMR, 10 STRUCTURES) IPAA 6	SP1F2; CHAIN: NULL;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;
SEQFOL D score				55.20	
PMF score		0.03	0.00		0.48
Verify score		-0.25	-0.52		-0.08
Psi Blast		3.2e-05	1.1e-16	1.4e-20	1.4e-20
END		239	169	201	198
STAR T AA		212	105	411	117
CHAI N ID			∢	A	A
PDB ID		lsp2	1453	1453	1453
SEQ ID NO:		1859	1859	1859	1859

PDB annotation	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION REGULATION/DNA), RNA	POLYMERASE III, 2 TO AMEGINETICAL PRITE APPLIATIONS TRANS	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	IKANSCKIPIION INIIIAIION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;			TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				TFIIIA; CHAIN; A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				TFIIIA: CHAIN: A. D. 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	MILLALOR ELEMENT DINA;	CHAIN: A, B;
SEQFOL D score											98.99														
PMF score		0.10				0.33										0.01						0.45			
Verify score		-0.24				-0.01										-0.25						-0.00			
Psi Blast		1.4e-28				1.1e-28					1.1e-28					3.2e-16						3e-22			
END AA		239				275					237					178						220			
STAR T AA		105				117					20					98						110			
CHAI N ID		A				A					A					A						C			
PDB 1D		1tf6				11f6					14f6					1tf6					_	Iubd			
SEQ ID NO:		1859				1859					1859					1859						1859			

Str.   P.DB   CHA   STAR   AA   AA   Secre   Score   Decore   Coumpound   P.DB annotation   D.			Ì			_					_	T							Τ					
PDB   CHAI   STAR   END   Psi Blast   Verify   PMF   SEQFOL	PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TKANSCKIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGIII ATION(DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	KECUGINITION, 3 COMPLEX	(INAINSCRIFTION REGITTATION ONA)	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTFIN/DNA) FINE-FINGER GI I:	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)
PDB         CHAI         STAR         END         Psi Blast         Verify         PMF           Iubd         C         152         265         3.2e-22         -0.06         0.07           Iubd         C         86         198         3.2e-33         -0.27         0.98           Iubd         C         93         197         3.2e-33         -0.27         0.98           2adr         I17         171         3.2e-16         -0.05         0.37           2gli         A         106         199         6.4e-33         -0.22         0.33	Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A, B;			YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			YYI: CHAIN: C: ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				ADR1; CHAIN: NULL;			ZINC FINGER PROTEIN GLII;		
PDB         CHAI         STAR         END         Psi Blast         Verity           Iubd         C         152         265         3.2e-22         -0.06         0           Iubd         C         86         198         3.2e-33         -0.06         0           Iubd         C         93         197         3.2e-33         -0.27         0           2adr         117         171         3.2e-16         -0.05         0           2gli         A         106         199         6.4e-33         -0.22         0	SEQFOL D score						68.47																	
PDB         CHAI         STAR         END         Psi Blast           ID         NID         TAA         AA         Psi Blast           1ubd         C         152         265         3.2e-22         -4           1ubd         C         86         198         3.2e-33         -4           1ubd         C         86         198         3.2e-33         -4           2adr         117         171         3.2e-16         -4           2gli         A         106         199         6.4e-33         -4	PMF score		0.07									0.98							0.37			0.33		
PDB         CHAI         STAR         END         Psi           ID         N ID         T AA         AA         Psi           1ubd         C         152         265         3.2e           1ubd         C         86         198         3.2e           1ubd         C         93         197         3.2e           2adr         117         171         3.2e           2gli         A         106         199         6.4e	Verify score		-0.06									-0.27							-0.05			-0.22	_	
PDB         CHAI         STAR           ID         N ID         T AA           1ubd         C         152           1ubd         C         86           1ubd         C         86           2adr         117           2gli         A         106			3.2e-22				3.2e-33					3.2e-33							3.2e-16			6.4e-33		
PDB CHAI  ID NID  NID  1ubd C  1ubd C  2adr  2gli A	END AA		265				198					197							171			661		
PDB 10bd 11ubd 0 1ubd 0 2adr 2gli 1	STAR T AA		152				98	_		_		93							117			106		
	CHAI N ID		၁				ပ					C		_								¥		
SEQ DD NO: NO: 1859 1859 1859 1859 1859 1859 1859 1859	PDB ID		1ubd				1 ubd					1ubd							2adr			2gli		
	SEQ ID NO:		1859				1859					1859							1859			1859		

ound PDB annotation	OTEIN GLII; COMPLEX (DNA-BINDING CHAIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	OTEIN GLII; COMPLEX (DNA-BINDING CHAIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	ER PEPTIDE; COMPLEX (ZINC FINGER/DNA)  EX  COMPLEX (ZINC FINGER/DNA),  IDE BINDING  ZINC FINGER, DNA-BINDING  DE OCTERN				
Coumpound	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score	68.84			69.01			64.40
PMF score		0.04	1.00		0.41	1.00	
Verify score		0.04	0.37		-0.35	0.40	
Psi Blast	6.4e-33	1.3e-31	4.8e-32	4.8e-32	3.2e-28	1.3e-37	1.3e-37
END	238	237	452	453	488	126	126
STAR T AA	83	96	371	372	399	4	ιν.
CHAI N ID	A	A	A	A	A	¥	A
PDB ID	2gli	2gli	lalh	1a1h	lalh	Ibuo	1buo
SEQ ID NO:	1859	1859	1860	1860	1860	1860	1860

SEQ	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
										CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1860	1mey	2	336	423	1.6e-47	-0.44	0.09		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRISIAL SIRUCIORE, COMPLEA (ZINC FINGER/DNA)
1860	lmey	ပ	370	452	1.3e-50	0.14	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN-DNA
-									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1860	lmey	၁	370	452	1.3e-50			67.59	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
					•				PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
,	Į,		100							(ZINC FINGER/DINA)
1860	Imey	ပ	398	488	3.2e-47	-0.16	0.71		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
									į	CRYSTAL STRUCTURE, COMPLEX
1020	1+3		000	400		9	6		THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE COMPANY OF THE CO	(ZINC FINGEN DINA)
1800	CIN	∢	399	488	3.2e-19	-0.48	0.23		TRANSCRIPTION FACTOR IIIA;	COMPLEX (TRANSCRIPTION PEGIT ATTOMONA) TENTA: 65
					-				CHAIN: F. F.	GENE NAR TEIIA PROTEIN DNA
										TRANSCRIPTION FACTOR, 5S RNA 2
										GENE, DNA BINDING PROTEIN
					•					ZINC FINGER, COMPLEX 3
										(TRANSCRIPTION
										REGULATION/DNA)
1860	1tf6	A	371	490	1.6e-31	-0.38	0.11		TFIIIA; CHAIN: A, D; 5S	COMPLEX (TRANSCRIPTION
									RIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX
									CHAIN: B, C, E, F;	(TRANSCRIPTION

SEQ ID	PDB U	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
NO:										REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTFIN
1860	lubd	U	344	448	1.16-32	-0.05	0.92		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	1ubd	O	375	488	6.4e-34	-0.03	0.89		YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	1ubd	ပ	406	493	4.8e-24	-0.08	0.10		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1860	2gli	∢	224	313	1.6e-09	0.05	-0.20		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1860	2gli	A	319	452	6.4e-34	0.10	0.07		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	REPLICATION DNA NUCLEOTIDE EXCISION REPAIR, UVRABC, HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN		TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB; CHAIN: A;	EUKARYOTIC INITIATION FACTOR 4A; CHAIN: A;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;
SEQFOL D score							٠					113.24
PMF		0.11	0.18	0.46	0.39	0.24	0.55	-0.14	0.43	,	1.00	
Verify score		-0.09	0.13	0.05	-0.11	-0.27	0.23	0.09	0.06		0.35	
Psi Blast		1.6e-34	1.6e-13	1.6e-13	1.4e-07	6.4e-17	9.6e-39	<b>4.8e-</b> 43	3.2e-91		7.5e-64	7.5e-64
END		490	630	630	662	859	029	321	029		211	217
STAR T AA	! !	344	470	470	238	457	508	105	313		4	15
CHAI N ID		A	A	А	A	A	A	Ą	В		¥	A
PDB ID		2gli	1c40	1d2m	1d2m	1d9x	1 fuk	1fuu	1 fuu		Ibyu	1byu
SEQ ID NO:		1860	1861	1861	1861	1861	1861	1861	1861	,	1862	1862

PDB annotation		TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN PROTEIN- N: PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	
Coumpound		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B:	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	RAB6 GTPASE; CHAIN: A;	GTP-BINDING PROTEIN YPT51; CHAIN: A;
SEQFOL	D score		109.68		102.67		98.76	95.76		
PMF	score	00.1		00'1		1.00			1.00	1.00
Verify	score	0.44		0.51		0.65			0.56	0.68
Psi Blast		1.3e-65	1.3e-65	8e-65	8e-65	6.4e-64	6.4e-64	3.2e-58	3.2e-62	9.6e-60
END	AA	211	215	181	181	182	182	182	179	179
STAR	TAA	6	6	91	17	17	17		18	18
CHAI	N ID	В	В	¥	A	А	A	¥	A	A
PDB	Œ	1byu	1byu	1c1y	lcly	lctq	1ctq	1cxz	1 <b>d</b> 5c	1ek0
SEQ	NO:	1862	1862	1862	1862	1862	1862	1862	1862	1862

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
A Ö	<u>e</u>	NID	T AA	AA		score	score	D score		
										HYDROLASE
1862	libr	Ą	17	187	3e-60			113.50	RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN
									BETA SUBUNIT; CHAIN: B, D;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1862	1 ibr	¥	18	186	3e-60	08.0	1.00		RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN
									BETA SUBUNIT; CHAIN: B, D;	BETA, P95 SMALL GTPASE,
										NUCLEAR TRANSPORT RECEPTOR
1862	1kao		17	182	9.6e-59			98.96	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-
										BINDING PROTEIN, SMALL G
1862	1	ر	5	108	1 46-60			11115	PAN: CHAIN: A C: MICI BAD	COMPLEY (SMATT
		>	3	2	000			C+.+11	DODE COME EX DECTED	COMPLES (SMALL)
									FORE COMPLEX FROIEIN	COMPLEY (SMALL)
									, 'a', Circuit, b',	COMIT LEA (SIVIALL
						_				GIPASE/NUCLEAR PROTEIN),
										SMALL GTPASE, 2 NUCLEAR
,				1						TKANSPORT
1862	Irrp	၁	16	193	1.4e-60	0.45	0.0		RAN; CHAIN: A, C; NUCLEAR	COMPLEX (SMALL
•									PORE COMPLEX PROTEIN	GTPASE/NUCLEAR PROTEIN)
					=				NUP358; CHAIN: B, D;	COMPLEX (SMALL
										GTPASE/NUCLEAR PROTEIN),
		•								SMALL GTPASE, 2 NUCLEAR
										TRANSPORT
1862	1tx4	M	19	180	4.8e-55			87.88	P50-RHOGAP; CHAIN: A;	COMPLEX(GTPASE
									TRANSFORMING PROTEIN	ACTIVATN/PROTO-ONCOGENE)
					-				RHOA; CHAIN: B;	GTPASE-ACTIVATING PROTEIN
										RHOGAP; COMPLEX (GTPASE
										ACTIVATION/PROTO-ONCOGENE),
										GTPASE, 2 TRANSITION STATE, GAP
1862	1zbd	¥	12	187	4.8e-69			130.15	RAB-3A; CHAIN: A;	COMPLEX (GTP-
									RABPHILIN-3A; CHAIN: B;	BINDING/EFFECTOR) RAS-RELATED
			•		***************************************					PROTEIN RAB3A; COMPLEX (GTP-
		_								BINDING/EFFECTOR), G PROTEIN,
										EFFECTOR, RABCDR, 2 SYNAPTIC
										EXOCYTOSIS, RAB PROTEIN,

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
NO:	1	OI N	I AA	AA		score	score	D score		
										RAB3A, RABPHILIN
1862	1zbd	∢	4	185	4.8e-69	0.65	1.00		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED
										PROTEIN RAB3A; COMPLEX (GTP-
										BINDING/EFFECTOR), G PROTEIN,
										EFFECTOR, RABCDR, 2 SYNAPTIC
										EXOCYTOSIS, RAB PROTEIN,
									A STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STA	RAB3A, RABPHILIN
1862	3rab	¥	13	182	8e-70	0.78	1.00		RAB3A; CHAIN: A;	HYDROLASE G PROTEIN,
										VESICULAR TRAFFICKING, GTP
										HYDROLYSIS, RAB 2 PROTEIN,
				******	•					NEUROTRANSMITTER RELEASE,
										HYDROLASE
1862	3rab	¥	13	182	8e-70			145.01	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN,
										VESICULAR TRAFFICKING, GTP
										HYDROLYSIS, RAB 2 PROTEIN,
										NEUROTRANSMITTER RELEASE,
									The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon	HYDROLASE
				1						
1864	la9n	Д	135	202	7.5e-07	0.40	0.52		U2 RNA HAIRPIN IV; CHAIN: Q, B: 112 A'; CHAIN: A	COMPLEX (NUCLEAR
_									A, 02 A, CIMIN. A, C, 02 B;	FROIEIN/KINA) COMFLEA
									CHAIN: B, D;	(NUCLEAK PROTEIN/RNA), RNA, SNRND BIRONTCI EODBOTEIN
1864	1b7f	A	138	207	3e-07	0.08	0.43		SXI. LETHAL PROTEIN: CHAIN:	RNA-BINDING PROTFIN/RNA TRA
									A. B: RNA (5'-	PRE-MRNA: SPI ICING
									R(P*GP*UP*UP*GP*UP*UP*UP*	REGULATION, RNP DOMAIN, RNA
									UP*UP*UP*UP*U)- CHAIN: P, Q;	COMPLEX
1864	lcvj	A	138	205	7.5e-07	0.47	0.57		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
									PROTEIN 1; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
									E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
									R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
									AP*AP*AP*A)-3'); CHAIN: M, N,	
									O, P, Q, R, S, T;	
1864	lcvj	ഥ	136	199	7.5e-07	0.54	0.43		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)

PDB annotation	BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS		RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	NUCLEOLIN RBD1; CHAIN: A;	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score	·						
PMF		0.21	66.0	0.15	0.43	0.95	0.48
Verify		0.48	0.13	0.20	0.05	0.32	0.38
Psi Blast		6c-07	1e-08	<b>20-99</b>	e-07	7.5e-07	3e-07
END		196	195	196	195	196	207
STAR T AA		136	135	88	136	138	138
CHAI N ID		¥	м	A		A	А
PDB ID		167	Inrc	1qm9	2ula	2up1	3sxl
SEQ NO:		1864	1864	1864	1864	1864	1864

PDB annotation	SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION			COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN	COMPLEX (TRANSCRIPTION FACTOR/DNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA-BINDING PROTEIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH
Coumpound	i	LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	:	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;
SEQFOL D score							
PMF score		0.01		0.60	0.47	0.43	0.60
Verify score		-0.21		-0.88	0.90	0:30	0.15
Psi Blast		3.2e-05		1.6e-21	1.2e-37	8e-08	1.4e-08
END		542		94	96	350	338
STAR T AA		439		-	,	183	209
CHAI N ID		∢		∢	A		Ą
PDB ID		Ises		1xbr	lxbr	1a4y	1a4y
SEQ ID NO:		1865		1867	1867	1870	1870

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										3 REPEATS
1870	1a4y	Ą	209	373	3e-06	0.14	0.25		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE),
									CHAIN: B, E;	COMPLEX (RI-ANG), HYDROLASE 2
										MOLECULAR RECOGNITION,
										EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1870	140b	A	196	333	8e-07	0.40	0.12		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH
										REPEAT, CALCIUM BINDING, CELL ADHESION
1870	140b	A	222	354	96000.0	-0.10	0.25		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH
										REPEAT, CALCIUM BINDING, CELL ADHESION
1870	1fo1	A	193	306	1.1e-06	0.03	0.03		NIICLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NEX.1)
									FACTOR 1: CHAIN: A. B:	RIBONICL EOPROTEIN (RNP.RBD
										OR RRM) AND LEUCINE-RICH-
										REPEAT 2 (LRR)
1870	1fo1	ф	193	306	1.1e-06	-0.01	0.00		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);
									FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP,RBD
						·				OR RRM) AND LEUCINE-RICH-
										REPEAT 2 (LRR)
1870	1fqv	٧	128	349	1.1e-46	0.45	0.51		SKP2; CHAIN: A, C, E, G, I, K, M,	LIGASE CYCLIN A/CDK2-
									O; SKP1; CHAIN: B, D, F, H, J, L,	ASSOCIATED PROTEIN P45; CYCLIN
									Ŋ, P;	A/CDK2-ASSOCIATED PROTEIN P19;
										SKP1, SKP2, F-BOX, LRR, LEUCINE-
										RICH REPEAT, SCF, UBIQUITIN, 2
										E3, UBIQUITIN PROTEIN LIGASE
1870	1fs2	∀	128	349	4.8e-36	0.22	0.72		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-
										ASSOCIATED P19; SKP1, SKP2, F-
										BOX, LRRS, LEUCINE-RICH
										REPEATS, SCF, 2 UBIQUITIN, E3,
1										UBIQUITIN PROTEIN LIGASE
1870	lyrg	А	248	347	0.00064	60.0	0.27		GTPASE-ACTIVATING	TRANSCRIPTION RNA1P; RANGAP;

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
			I AA	AA		score	score	D score		
									PROTEIN RNA1_SCHPO; CHAIN; A. B:	GTPASE-ACTIVATING PROTEIN FOR SPII, GTPASE-ACTIVATING
						-				PROTEIN, GAP, RNAIP, RANGAP,
						-				LRR, LEUCINE- 2 RICH REPEAT
										PROTEIN, TWINNING,
_										HEMIHEDRAL TWINNING, 3
										MEROHEDRAL TWINNING,
_										MEROHEDRY
1870	2bnh		209	338	3.2e-09	-0.03	0.71		RIBONUCLEASE INHIBITOR;	ACETYLATION RNASE INHIBITOR,
									CHAIN: NOLL;	KIBONUCLEASE/ANGIOGENIN
					·					INHIBITOR ACETYLATION,
$\dagger$							,			EEOCINE-MOI NELEVIS
1871	1bak		168	291	4.8e-10	0.08	-0.03		G-PROTEIN COUPLED	TRANSFERASE GRK-2, BETA-
									RECEPTOR KINASE 2; CHAIN:	ADRENERGIC RECEPTOR KINASE 1,
									NULL;	BETA-ARK PLECKSTRIN
										HOMOLOGY DOMAIN, PH DOMAIN,
										SIGNAL TRANSDUCTION, 2 G-
										BETA-GAMMA BINDING DOMAIN,
										BETA-ADRENERGIC RECEPTOR 3
-										KINASE, BETA-ARK, G-PROTEIN
	-									COUPLED RECEPTOR KINASE (GRK-
+	Ibtn		172	271	8e-12	0.19	96.0		BETA-SPECTRIN: 1BTN 4	2) SIGNAT TRANSDITCTION PROTEIN
							! !		CHAIN: NULL; 1BTN 5	
_	1dro		182	264	1.5e-05	0.22	0.21		BETA-SPECTRIN; 1DRO 6	CYTOSKELETON
-									CHAIN: NULL; 1DRO 7	
_	1dyn	Ą	186	271	4.8e-10	0.13	0.11		SIGNAL TRANSDUCTION	
		_							PROTEIN DYNAMIN	
									(PLECKSTRIN HOMOLOGY	
$\dashv$									DOMAIN) (DYNPH) 1DYN 3	
1871	lefi	<b>∀</b>	149	464	1.6e-58	0.05	0.53		MOESIN; CHAIN: A, B; MOESIN;	MEMBRANE PROTEIN CRYSTAL
									CHAIN: C, D;	STRUCTURE, MEMBRANE, FERM DOMAIN TAIL DOMAIN
1										DOMEIN, THIE DOMEIN

CHAI N ID	1	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
A 170	170		269	3.2e-17	0.31	0.80		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNALING PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
A 170	17	0	269	3.2e-17	0.14	69.0		DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	SIGNATOR PROTEIN DAPP1, PHISH, BAM32; PLECKSTRIN, 3-PHOSPHOINOSITIDES, INOSITOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN, ADAPTOR PROTEIN
A 15	2	172	272	4.8e-18	0.49	0.65		GRP1; CHAIN: A;	SIGNALING PROTEIN ARFI GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN
A		134	464	3.2e-58	-0.01	0.01		RADIXIN; CHAIN: A;	CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION
16	16	691	285	1.4c-14	0.14	0.09		PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY DOMAIN) MUTANT 1PLS 3 WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS 1PLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) 1PLS 5	
A S			390	0			69.11	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS
A 8	∞		387	0	0.03	0.54		3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,

					1										_				_				
PDB annotation	DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	OXIDOREDUCTASE OXALOSUCCINATE	DECARBOXYLASE, IDH; OXIDOREDUCTASE (NAD(A)-	CHOR(L)), NADF, PHOSPHORYLATION, 2 GLYOXYLATE BYPASS	OXIDOREDUCTASE OXALOSUCCINATE	DECARBOXYLASE, IDH;	CHOH(D)), NADP,	PHOSPHORYLATION, 2	OLIOAILAIE BIFASS	OXIDOREDUCTASE IFMDH, IMDH;   OXIDOREDUCTASE.	DEHYDROGENASE, NAD-	DEPENDANT ENZYME, 2 LEUCINE	BIOSYNTHETIC PATHWAY	OXIDOREDUCTASE IPMDH, IMDH;	OXIDOREDUCTASE,	DEHYDROGENASE, NAD-	DEPENDANT ENZYME, 2 LEUCINE	BIOSYNTHETIC PATHWAY	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDIICTASE	DEHYDROGENASE, LEUCINE	BIOSYNTHETIC PATHWAY, 2 NAD-	DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,
Coumpound	B;	ISOCITRATE DEHYDROGENASE; CHAIN:	NULL;		ISOCITRATE DEHYDROGENASE; CHAIN:	NULL;			2 16 Opp Opy 1444 ATE	DEHYDROGENASE: CHAIN: A.	B;			3-ISOPROPYLMALATE	DEHYDROGENASE; CHAIN: A,	B;		יייייייייייייייייייייייייייייייייייייי	3-ISOPROPYLMALATE DEHYDROGENASE: CHAIN: A.	B;			3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,
SEQFOL D score					62.58				02 67	02.70								2	60.42				
PMF score		09.0												0.41									0.65
Verify score		0.01												0.04									-0.04
Psi Blast		0			0					>				0					o				0
END AA		387			387				362	786				389				300	282				389
STAR T AA		5			7				-	-1													_
CHAI N ID									-	¢				¥				<	₹				A
PDB ID		1ai2			1ai2				10m7	11121				1cm7				1007	ıcuz				lcnz
SEQ ID NO:		1872			1872				1877	701				1872				1877	7/01				1872

		r			T		T		
PDB annotation	DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME	OXIDOREDUCTÁSE IPMDH; 1IDM 7 CHIMERA 1IDM 20	OXIDOREDUCTASE IPMDH; 1IDM 7 CHIMERA 1IDM 20	OXIDOREDUCTASE IPMDH, IMDH; 1XAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21	OXIDOREDUCTASE IPMDH, IMDH; IXAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLMALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPFAT	COMPLEX (TRANSCRIPTION
Coumpound	В;	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	3-ISOPROPYLMALATE DEHYDROGENASE; 1IDM 5 CHAIN: NULL; 1IDM 6	3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE 2T2M6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA:
SEQFOL D score		54.18		50.68			68.62		
PMF score		<u>.</u>	0.42		0.46	0.57		0.51	0.22
Verify score			0.06		0.04	-0.03		0.44	0.11
Psi Blast		4.8e-95	4.8e-95	1.6e-96	1.6e-96	0	0	1.6e-23	4.8e-36
END AA		366	387	366	387	387	388	125	156
STAR T AA		42	6	42	6	9	9	01	10
CHAI N ID						A	<b>∀</b>		В
PDB ID		lidm	lidm	lxac	lxac	2ayq	2ayq	la5e	lawc
SEQ ID NO:		1872	1872	1872	1872	1872	1872	1873	1873

PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR.	ANKYRIN MÓTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR,	ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK4A,	MTSI; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN	CDK, INK4, CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/AN II- ONCOGENE) HEADER	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL:	,	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE	TUMOR SUPPRESSOR; CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B.
SEQFOL D score																		
PMF score			1.00			0.11		96.0		0.62						0.15		
Verify score			0.43			0.05		0.22		0.52						0.18		
Psi Blast			6.4e-33			3.2e-32		1.1e-23		8e-24						8e-33		
END			125			157		128	,	125						157		
STAR T AA			2	·		13		m		0 ———	_					13		
CHAI N ID		_	В						ļ	Я						В		
PDB ID			lawc			1bd8		1bd8		lbi7						1blx		
SEQ El	2		1873			1873		1873	OHO.	1873						1873		

PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	FROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	P18NK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONF/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HOKMUNE/GROW I H FACTOR	SIGNALING PROTEIN HELIX-TURN-	CELL CYCLE INHIBITOR P18.	INK4C(INK6): CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	ANK-REPEAT MYOTROPHIN,	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	B;		CYCLIN-DEPENDENT KINASE	o manifold, curaint. P.,		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN; A. B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				MYOTROPHIN; CHAIN: NULL	NF-K APPA-B P65: CHAIN: A C:	NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score																										
PMF score		96'0			0.71			0.55			,		0.49	0.60	3				0.74					0.64	0.45	0.45
Verify score		0.42			0.16			0.15					0.05	0.23					0.14					0.21	0.00	0.02
Psi Blast		1.6e-22			6.4e-34			4.8e-27					3.2e-24	6.4e-34					1,6e-26		-			1.3e-24	3.26-40	27.7
END		128			153			130					131	153	)				129					127	212	717
STAR T AA		т			10			2					9	10	) 1				7						4	-
CHAI N ID		В			Ą			A					Ą	A	<u>:</u>				А						ĹΤ	1
PDB ID		1blx			1bu9			1bu9					1d9s	1ihb					liho					1myo	Infi	
SEQ ID NO:		1873			1873			1873					1873	1873					1873					1873	1873	

	NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
								I-KAPPA-B-ALPHA; CHAIN: E, F;	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
$\vdash \vdash$		10	000	20016	,,,	100		Trib (Ob crimbrecon	TIDAE THE TREE PARTY
		2	071	3.26-16	0.03	0.81		TOMOK SUPPRESSOR PI6INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1bd8		13	153	3.2e-27	0.03	0.31		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1bd8		2	120	1.4e-15	-0.04	0.01		P19INK4D CDK4/6 INHIBITOR; CHAIN; NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1bi7 B		10	120	3.2e-17	0.18	99.0		CYCLIN-DEPENDENT KINASE	COMPLEX (KINASE/ANTI- ONCOGENE) CDK 6: PIENIX 4A
<del></del> .								TUMOR SUPPRESSOR; CHAIN:	MTSI; CYCLIN DEPENDENT
								В;	KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN
									CDK, INK4, CELL CYCLE, MULTIPLE
	_			_					TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-
									ONCOGENE) HEADER
lbi7 B	<u> </u>	52	153	1.4e-17	0.15	0.00		CYCLIN-DEPENDENT KINASE	COMPLEX (KINASE/ANTI-
					, -			6; CHAIN: A; MULTIPLE TIMOR SUPPRESSOR: CHAIN:	ONCOGENE) CDK6; P16INK4A, MTS1: CYCLN DEPENDENT
								B;	KINASE, CYCLIN DEPENDENT
									KINASE INHIBITORY 2 PROTEIN,
									CDK, INK4, CELL CYCLE, MULTIPLE
									COMPLEX (KINASE/ANT).
							1		ONCOGENE) HEADER
1blx B	3	13	153	3.2e-25	0.09	0.31		CYCLIN-DEPENDENT KINASE	COMPLEX (INHIBITOR
								6; CHAIN: A; P19INK4D; CHAIN: B:	PROTEIN/KINASE) INHIBITOR PROTEIN CYCI IN DEBENDENT

 CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL Deserte	Coumpound	PDB annotation
 מו גו	1 88	WW .		30016	21036	alos o		
								KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
 В	2	120	1.6e-14	90.0	-0.09		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
							B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL,
								ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
 A	13	158	1.3e-29	-0.15	0.23		CYCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-
							6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR,
 _								CYCLIN-2 DEPENDENT KINASE,
								HORMONE/GROWTH FACTOR
A	2	125	1.3e-18	0.04	0.11		CYCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-
							6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR,
								CYCLIN-2 DEPENDENT KINASE.
								HORMONE/GROWTH FACTOR
¥	54	212	6.4e-28	0.01	0.05		CYCLIN-DEPENDENT KINASE	HORMONE/GROWTH FACTOR P18-
							6 INHIBITOR; CHAIN: A;	INK4C; CELL CYCLE INHIBITOR,
								P18INK4C, TUMOR, SUPPRESSOR,
								CICLIN- Z DEFENDENT KINASE, HORMONE/GROWTH FACTOR
A	10	120	1.6e-17	0.28	0.33		CYCLIN-DEPENDENT KINASE	SIGNALING PROTEIN HELIX-TURN.
							4 INHIBITOR B; CHAIN: A;	HELIX, ANKYRIN REPEAT
Ą	13	122	1.5e-12	0.08	69:0		PYK2-ASSOCIATED PROTEIN	METAL BINDING PROTEIN ZINC-
							BETA; CHAIN: A;	BINDING MODULE, ANKYRIN
								REFEATS, METAL BINDING PROTEIN
A	2	124	4.8e-18	0,40	0.71		CYCLIN-DEPENDENT KINASE	CELL CYCLE INHIBITOR P18-
							6 INHIBITOR; CHAIN: A, B;	INK4C(INK6); CELL CYCLE
								INHIBITOR, P18-INK4C(INK6),
								ANKYRIN REPEAT, 2 CDK 4/6

	,			. —		 			
PDB annotation	INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	P53; CHAIN: A; 53BP2; CHAIN: B;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score								72.03	
PMF score		0.27	0.24	0.23	0.01	99.0	0.00		60.0
Verify score		-0.09	-0.17	0.30	-0.03	0.12	0.04		-0.14
Psi Blast		3.26-27	1.1e-21	1.1e-21	4.8e-20	9.6e-26	7.5e-29	7.5e-29	1.5e-39
END		211	138	159		335	336	365	502
STAR T AA		54	11	73	09	239	243	283	395
CHAI N ID		A			д	Æ	A	A	A
PDB ID		lihb	Imyo	1myo	1ycs	lalh	1a1h	lalh	la1h
SEQ ID NO:		1874	1874	1874	1874	1877	1877	1877	1877

PDB CHAI STAR END ID NID TAA AA	STAR T AA	ļ	END	r	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
Imey         C         161         263         4.8e-42         -0.16	161 263 4.8e-42	263 4.8e-42	4.8e-42		-0.16		90.0		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
						_			PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
								:		CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
lmey C 166 307 le-11 -0.57	166 307 le-11	307 le-11	le-11		-0.57		00.0		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
				<del>-</del> -					PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1mev C 100 335 32-26 -0.46	100 33% 30-76	335 30-76	36-26		-0.46		037		DNA: CHAM: A B B E.	COMPLEY (TRIC FINGER/DNA) ZING
27-20	07-07	07-20	07-20		2		(5.0		CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1mey C 217 307 8e-40 -0.24	217 307 8e-40	307 8e-40	8e-40		-0.24		0.07		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
	,	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	,	1						(ZINC FINGEK/DNA)
1mey C 266 335 1.3e-39 0.02	266 335 1.3e-39	335 1.3e-39	1.3e-39		0.02		0.95		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									DROTEIN: CHAIN: C E G.	FINGER, FROIEIN-DINA INTER A CTION DE OTEN 2
								•	110 tem, Circuit. C, 1, C,	CRYSTAL STRICTIME COMPLEX
										(ZINC FINGER/DNA)
1mey C 282 363 6.4e-50 0.29	282   363   6.4e-50	363 6.4e-50	6.4e-50		0.29		1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROFEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER (DNA)
Imey C 282 364 8e-51	282 364	364		8e-51				98.05	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
ΒÖ	3	9	I AA	AA		score	score	D score		
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	2	310	391	8e-51	60'0	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER PROTEIN-DNA
									PROTEIN; CHAIN; C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1mey	Ü	338	419	3.2e-51	0.43	1.00		DNA; CHAIN; A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSOS ZINC FINGER	FINGER, PROTEIN-DNA INTERACTION PROTEIN DESIGN 2
٠					-			,	, (1, 0, 1), (1, 1, 1), (1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1	CRYSTAL STRUCTURE, COMPLEX
1	,									(ZINC FINGER/DNA)
1877	1mey	ပ	366	447	1.3e-50	0.28	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSOS ZINC FINGER PROTEIN: CHAIN: C. F. G:	FINGER, PROTEIN-DNA INTERACTION. PROTEIN DESIGN. 2
	-									CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1877	Imey	Ü	394	473	4.8e-47	0.20	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
				•		•			PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
····,										CRYSTAL STRUCTURE, COMPLEX
1077	1		200	†	0.7	000	5		0 0 0	(ZINC FINGER/DINA)
18//	Imey	ر	77.5	675	3e-40	-0.02	0.82		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSOS ZINC FINGER	FINGER, PROTEIN-DINA
									FNO IEIN, CIMIN, C, F, G,	OBYGEAU GEBIGEINDESIGN, Z
										CRISIAL SIRUCIURE, COMPLEX
U	,	,		T						(ZINC FINGER/DNA)
1877	lmey	ပ	450	529	3.2e-48	0.39	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
				-	-					CRYSTAL STRUCTURE, COMPLEX
1	,			1					and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s	(ZINC FINGER/DNA)
1877	lmey	2	476	533	8e-34	0.46	1.00		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a ö	A	N ID	TAA	AA		score	score	D score		
		-							CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	Imey	9	187	214	1.6e-11	-0.12	0.48		DNA; CHAM: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	Imey	Ð	236	263	6.4e-12 .	-0.05	0.52		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1877	1sp2		190	218	9.6e-07	0.02	0.09		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1877	14f3	A	239	335	4.8e-17	0.27	0.07		TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1877	11f6	A	162	316	8e-31	-0.24	0.11		TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1877	14f6	А	239	400	9.6e-36	-0.06	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

PDB annotation	(TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION
	(TRANSCRIPTION REGULATION/DN. POLYMERASE III, TRANSCRIPTION I	COMPLEX (TRAN) REGULATION/DN (TRANSCRIPTION) REGULATION/DN POLYMERASE III, TRANSCRIPTION FINGER PROTEIN	COMPLEX (TRANS REGULATION/DN/ (TRANSCRIPTION REGULATION/DN/ POLYMERASE III, TRANSCRIPTION I	COMPLEX (TRANS REGULATION/DNA (TRANSCRIPTION REGULATION/DNA POLYMERASE III, 2 TRANSCRIPTION II	COMPLEX (TRANS REGULATION/DNA (TRANSCRIPTION REGULATION/DNA POLYMERASE III, 2 TRANSCRIPTION IN	COMPLEX
Coumpound	CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	YY1; CHAIN: C; ADENO-
SEQFOL D score		107.85				
PMF score			0.99	1.00	0.95	0.37
Verify score			-0.02	0.12	0.17	-0.39
Psi Blast		7.5e-68	86-38	4.8e-38	8e-34	1.4e-26
END		471	454	511	531	335
STAR T AA		310	311	367	395	165
CHAI N ID		A	¥	A	¥	၁
PDB ID		1476	1476	1476	1tf6	lubd
SEQ ID NO:		1877	1877	1877	1877	1877

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	lubd	ပ	243	363	7.5e-40	-0.00	0.98		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	lubd	ပ	246	363	6.4e-33	-0.09	0.86		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	၁	287	391	36-50	0.00	00.1		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1877	1ubd	O	318	419	3.2e-35	-0.13	0.95		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION,

PDB annotation	INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound	CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY I; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score		86.32			
PMF score			0.99	0.95	66.0
Verify score			0.26	0.03	0.10
Psi Blast		3e-48	1.1e-47	4.8e-32	3e-48
END		448	474	473	501
STAR T AA		340	364	374	392
CHAI N ID		O	C	S	၁
PDB ID		1ubd	1ubd	1ubd	1ubd
SEQ ID NO:		1877	1877	1877	1877

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PDB annotation		RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	FINITE DE PROTEIN DNA PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADR1, ZINC FINGER, NMR	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound			YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	Chain: A, b;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					ADR1; CHAIN: NULL;			ADR1; CHAIN: NULL;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;			ZINC FINGER PROTEIN GLI1;	CHAIN: A; DNA; CHAIN: C, D;		** *** * ** ** ** ** ** ** ** ** ** **	ZINC FINGER PROTEIN GLII:
SEQFOL	D score																															93.76
PMF	score		1.00							1.00	,							0.41			0.63			0.80				0.41				
Verify	score		0.12							-0.08								-0.48			-0.23			0.15				0.19				
Psi Blast			1.5e-48							8e-34								1.3e-14			I.6e-12			1.5e-46				3.2e-33			,	1.5e-66
END	AA		530							529								216			309			365				390				421
STAR	I AA		420		,					430								162			239			061				246			000	787
CHAI	OI N		၁							ပ														A				Ą				Ą
PDB	a l		1ubd							1ubd								2adr			2adr			2gli				2gli				7g11
SEQ	NO:		1877							1877				<u> </u>				1877			1877			1877				1877			1077	18//

1 PDB annotation	JN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)			E- HEXAMERIZATION DOMAIN ROTEIN; HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT					ļ`	OSPHATE TRANSFERASE CK; NUCLEOTIDE
EQFOL Coumpound D score	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A:	N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A:	HEAT SHOCK PROTEIN HSLV; CHAIN: A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN: E, F:	CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	HEAT SHOCK PROTEIN HSLU; CHAIN: A:	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CYTIDINE MONOPHOSPHATE
<u> </u>				65.03						
PMF score		0.27	0.93		0.64	0.10	0.28	0.57	0.23	0.15
Verify		-0.16	-0.16		0.35	-0.74	0.22	0.00	0.16	-0.51
Psi Blast		1.5e-66	66-53	3.2e-15	3.2e-15	3.2e-13	1.5e-15	1.6e-16	4.5e-34	0.0045
END AA		503	533	424	349	270	405	360	442	245
STAR T AA		310	395	169	961	691	184	169	183	218
CHAI N ID		A	А	A	A	त्म	A	A	A	4
PDB ID		2gli	2gli	1d2n	1d2n	1e94	Ifnn	1g41	1g41	2cmk
SEQ ID NO:		1877	1877	1878	1878	1878	1878	1878	1878	1878

score D score  77.13 ASPARTATE AMINOTRANSFERASE; CHAIN: A, B; ASPARTATE AMINOTRANSFERASE; CHAIN: A, B; AMINOTRANSFERASE; CHAIN: A, B; AMINOTRANSFERASE; CHAIN: A, B; TRANSFERASE(AMINOTRANSF
76.94 TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXED WITH 1ARS 3 PYRIDOXAL-5'- PHOSPHATE 1ARS 4
71.45 TRYPTOPHANASE; CHAIN: A, B, C, D;
1.00 I-AMINOCYCLOPROPANE-I- CARBOXYLATE SYNTHASE; CHAIN: A. B:
0.33 3-AMINO-5-

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
NO:	OI	NID	TAA	AA		score	score	D score		
						!			HYDROXYBENZOIC ACID SYNTHASE; CHAIN: A;	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)
1882	1bjw	A	102	515	9.6e-84	0.52	1.00		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME
1882	1bjw	A	83	514	9.6e-84			134.98	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME
1882	15w0	A	99	520	1.6e-67	0.24	1.00		TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP
1882	1bw0	A	92	520	1.6e-67			158.29	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP
1882	1c7n	A	125	514	6e-52	0.34	1.00		CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE
1882	lcs1	A	144	302	1.6e-08	-0.10	0.13		CYSTATHIONINE GAMMA- SYNTHASE; CHAIN: A, B, C, D;	LYASE CGS; LYASE, LLP. DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS
1882	1d2f	A	128	514	4.56-53	0.35	1.00		MALY PROTEIN; CHAIN: A, B;	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C- 2 TERMINAL DOMAIN, OPEN ALPHA-BETA STRUCTURE.
1882	Idfo	<b>4</b>	182	415	4.8e-07	0.42	00.1		SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD
1882	lelu	Ą	123	514	9.6e-13	0.17	0.87		L'CYSTEINE/L-CYSTINE C-S LYASE; CHAIN: A, B;	LYASE FES CLUSTER BIOSYNTHESIS, PYRIDOXAL 5'-

PDB annotation	PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME- PRODUCT COMPLEX			CHAIN: AMINOTRANSFERASE AROAT;	CHAIN: AMINOTRANSFERASE AROAT;	RANSF ST 3	RANSF ST 3	SE; LYASE LYASE, PLP-DEPENDENT ENZYME. PYRIDOXAL PHOSPHATE	+
Coumpound		ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B, C, D;	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A. B:	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5'-PHOSPHATE AND MALEATE 2CST 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5'-PHOSPHATE AND MALEATE 2CST 4	TYROSINE PHENOL-LYASE; CHAIN: A, B;	TYROSINE AMINOTRANSFERASE: CHAIN:
SEQFOL D score		79.51		74.67			75.00		
PMF			1.00		0.88	0.95		0.34	0.95
Verify			0.06		-0.16	-0.13		0.01	-0.17
Psi Blast		4.8e-52	4.8e-52	8e-53	8e-53	1.6e-58	1.6e-58	1.1e-48	9.6e-58
END		516	452	488	457	517	499	508	457
STAR T AA		92	68	62	85	81	88	110	08
CHAI N ID		A	A	Ą	Ą	A	A	A	A
PDB ID		1yaa	l yaa	2ay l	2ay1	2cst	2cst	2tpl	3tat
SEQ ID NO:		1882	1882	1882	1882	1882	1882	1882	1882

PDB annotation	SUBSTRATES, PLP ENZYME	AMINOTRANSFERASE PHEAT, TYRAT, AROAT; AMINOTRANSFERASE, AROMATIC SUBSTRATES, PLP ENZYME			HYDROLASE TYROSINE PHOSPHATEASE, LAR PROTEIN	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE DUAL SPECIFICITY PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE	HYDROLASE VHR; HYDROLASE, PROTEIN DUAL-SPECIFICITY PHOSPHATASE	IMMUNOGLOBULIN
Coumpound		TYROSINE AMINOTRANSFERASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'- PHOSPHATE AT PH 7.5 7AAT 4	LAR; CHAIN: A, B;	PYST1; CHAIN: NULL;	PYST1; CHAIN: NULL;	HUMAN VHI-RELATED DUAL- SPECIFICITY PHOSPHATASE CHAIN: A, B;	HUMAN VHI-RELATED DUAL- SPECIFICITY PHOSPHATASE CHAIN: A, B;	ANTIBODY CTM01; CHAIN: L,
SEQFOL D score	ı	91.42		78.03		68.80		139.04		
PMF score			0.43		0.18		1.00		1.00	1.00
Verify score			-0.10		-0.13		0.57		0.74	0.30
Psi Blast		9,6e-58	6.4e-65	6.4e-65	1.1e-58	6.4e-24	6.4e-24	7.5e-31	7.5e-31	9.6e-82
END		497	457	492	220	200	200	208	200	242
STAR T AA		95	73	88	3	52	55	37	50	20
CHAI N ID		A	A	A	В			¥	A	Н
PDB ID		3tat	7aat	7aat	Ilar	lmkp	Imkp	lvhr	lvhr	1ae6
SEQ ID NO:		1882	1882	1882	1883	1883	1883	1883	1883	1884

SEQ	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
NO:									ť	IMMUNOGLOBULIN, FAB
1884	lafv	Н	20	244	8e-84	0.43	1.00		HUMAN IMMUNODEFICIENCY	COMPLEX (VIRAL
									VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3	CAPSID/IMMUNOGLOBULIN) HIV-1 CA. HIV CA. HIV P24, P24; FAB. FAB
									FŘAGMENT; CHAIN: H, K, L, M;	LIGHT CHAIN, FAB HEAVY CHAIN
										CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1884	1bd2	ഥ	21	261	1.2e-81			301.81	HLA-A 0201; CHAIN: A; BETA-2	COMPLEX (MHC/VIRAL
									MICROGLOBULIN; CHAIN: B;	PEPTIDE/RECEPTOR) HLA A2
									TAX PEPTIDE; CHAIN: C; T	HEAVY CHAIN; COMPLEX
									CELL RECEPTOR ALPHA;	(MHC/VIRAL PEPTIDE/RECEPTOR)
									CHAIN: D; 1 CELL RECEFIOR BETA; CHAIN: E;	
1884	1bd2	ы	22	261	1.2e-81	99.0	1.00		HLA-A 0201; CHAIN: A; BETA-2	COMPLEX (MHC/VIRAL
									MICROGLOBULIN; CHAIN: B;	PEPTIDE/RECEPTOR) HLA A2
									TAX PEPTIDE; CHAIN: C; T	HEAVY CHAIN; COMPLEX
									CELL RECEPTOR ALPHA;	(MHC/VIRAL PEPTIDE/RECEPTOR)
									CHAIN: D; T CELL RECEPTOR	
									BETA; CHAIN: E;	
1884	1bec		21	261	1.5e-76			273.44	14.3.D T CELL ANTIGEN	RECEPTOR T CELL RECEPTOR 1BEC
		_							RECEPTOR; 1BEC 5 CHAIN: NULL: 1BEC 6	14
1884	1 <b>d5</b> i	H	20	244	1.3e-81	0.23	0.99		CHIMERIC GERMLINE	IMMUNE SYSTEM IMMUNE
									PRECURSOR OF OXY-COPE	SYSTEM
									CHAIN: L; CHIMERIC	
								-	GERMLINE PRECURSOR OF	
									OXY-COPE CHAIN: H;	
1884	le60	I	70	244	4.8e-81	0.40	1.00		IMMUNOGLOBULIN LIGHT	IMMUNOGLOBULIN FAB,
									CHAIN; CHAIN: L;	ANTIBODY, ANTIGEN, HIV-1, P24,
									IMMUNOGLOBULIN HEAVY	CA
,,,,,	,	6		!	,				CHAIN; CHAIN: H;	
1884	Itvd	В	20	247	1.1e-84	0.18	1.00		IMMUNOGLOBULIN FAB	

SEQ	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
a Š	<u>a</u>	O N	TAA	AA		score	score	D score		
									FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1884	lige	Н	20	247	1.6e-83	0.22	00'1		COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) 11GC 5 PROTEIN G, STREPTOCOCCUS 11GC 15	
1884	ligt	В	20	282	3.2e-90	-0.00	0.98		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1884	ligy	æ	21	282	3.2e-82	0.07	0.82		IGGI INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1884	lngp	Н	20	244	1.6e-83	0.21	1.00		NIG9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN,
1884	lnqb	A	12	130	9e-07	0.22	1.00		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1884	1tcr	В	19	262	8e-71			277.99	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1885	1841	A	314	369	0.0094	-0.34	0.04		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1886	Ibuo	Ą	01	129	4.8e-24	0.34	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2

PDB annotation	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) IPHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score										
PMF score		1.00	0.65	-0.20	-0.19	-0.19	0.54	1.00	66.0	0.55
Verify score		0.45	0.42	0.70	0.77	0.89	0.07	0.47	0.44	0.01
Psi Blast		4.5e-05	3e-05	4.5e-09	7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05	6e-05
END AA		1410	1417	207	218	204	1396	1410	1410	1432
STAR T AA		1342	1331	14	11	37	1325	1339	1342	1339
CHAI N ID		Ą	¥	⋖		Ą			Ą	Ą
PDB ID		1d8z	1fjc	losm	1pho	1994	lsxl	2sxl	2u2f	3sxl
SEQ ID NO:		1887	1887	1887	1887	1887	1887	1887	1887	1887

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF score	SEQFOL D score	Coumpound	PDB annotation
										SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1888	1b7f	A	1303	1371	9e-05	0.53	1.00		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP.	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1888	Icvj	A	1303	1371	3e-05	0.41	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*A):3'; CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1888	lcvj	В	1301	1371	3e-0 <i>5</i>	0.41	0.89		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1888	Id8z	А	1303	1371	4.5e-05	0.45	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1888	1fjc	Α _	1292	1378	3e-05	0.42	0.65		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1888	Iosm	¥	14	207	4.5e-09	0.70	-0.20		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
1888	1pho		11	218	7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
1888	1994	A	37	204	4.5e-08	0.89	-0.19		ALPHA-LYTIC PROTEASE;	HYDROLASE DOUBLE BETA

PDB annotation	BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound	CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C- TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2ÁF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP* UP*UP*UP*U)- CHAIN: P. O:	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP-3'); CHAIN: M, N, O, P, Q, R, S, T;
SEQFOL D score							
PMF score		0.54	1.00	0.99	0.55	1.00	1.00
Verify		0.07	0.47	0.44	0.01	0.53	0.41
Psi Blast		0.00015	0.00015	1.3e-05	6e-05	96-05	3e-0 <i>5</i>
END AA		1357	1371	1371	1393	1313	1313
STAR T AA		1286	1300	1303	1300	1245	1245
CHAI N ID				A	4	Ą	∢
PDB ID		1sxl	2sxí	2u2f	3sxl	167f	lcvj
SEQ ID NO:		1888	1888	1888	1888	1889	1889

GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA BINDING DOMAIN STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS OUTER MEMBRANE PROTEIN OSMOPORIN, OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE	
OUTER MEMBRANE PROTEI SMOPORIN, OUTER MEMB ROTEIN, NON-SPECIFIC PO SMOPORIN, 2 BETA-BARRI RANSMEMBRANE IYDROLASE DOUBLE BETA SARREL, BACTERIAL SERIN ROTEASE	OUTER MEMBRANE PROTEI SMOPORIN, OUTER MEMB ROTEIN, NON-SPECIFIC PO SMOPORIN, 2 BETA-BARRI RANSMEMBRANE IYDROLASE DOUBLE BETA BARREL, BACTERIAL SERIN ROTEASE
ROLASE DOUBLE BE REL, BACTERIAL SER TEASE	ROLASE DOUBLE BE REL, BACTERIAL SER TEASE
YDROLASE DOUB ARREL, BACTERLA ROTEASE	YDROLASE DOUB ARREL, BACTERLA ROTEASE
TERMÍNUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294	!A-   4 SXL   SXI,
ì	) ISXL
TANK STATE	MEI) ISXL IRES) ISXI.
SIDUES 199 - 20	(RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR. 17 STRUCTURES) 1SXL
RBD-2), RESI	RBD-2), RESI PLUS N-TERN 1 AMR, 17 ST
(RBD-2), RESIDUES 199 - 29	
_	

PDB annotation	PROTEIN RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION X CHROMOSOME	DOSAGE COMPENSATION RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOWALN, TRANSMEMBRANE, GI VCOPP OTTEN	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III		HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2
Coumpound	SEX-LETHAL; CHAIN: A, B, C;	GP130; CHAIN: NULL;	TITIN; CHAIN: NULL;	TITIN; CHAIN: NULL;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	FIBRONECTIN; CHAIN: A;	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;
SEQFOL D score						57.74	
PMF score	0.55	0.23	0.70	0.94	-0.18		-0.06
Verify	0.01	0.21	0.07	0.18	0.02		0.28
Psi Blast	6e-05	1.6e-12	9.6e-11	1.2e-12	1.6e-16	6.4e-28	9.6e-17
END AA	1335	262	265	266	355	450	348
STAR T AA	1242	991	165	591	162	168	168
CHAI N ID	A					A	Ą
PDB ID	3sxl	15j8	1bpv	1bpv	1cfb	1 fnh	1qg3
SEQ ID NO:	1889	1894	1894	1894	1894	1894	1894

PDB annotation	PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	CTIN TF 3	BNA BINING BROTHINBINA			, G; RNA-BINING PROTEIN, RNA BINDING PROTEIN/RNA				DED   PROTEIN DSRBD, DROSOPHILA,		שימייים יו ממ בטי מבו ייסטי טוני
Coumpound		TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	DOUBLE STRANDED BNA	BINDING PROTEIN A; CHAIN:	R(*GP*GP*CP*GP*CP*GP*CP*G	P*CP*C)-3'); CHAIN: C, D, E, G;	WWPROTOTYPE; CHAIN: A;	MATERNAL EFFECT PROTEIN	(STAUFEN); CHAIN: A;	STAUFEN DOUBLE-STRANDED	CHAIN: B;	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
SEQFOL D score															
PMF score		0.29	0.12	<b>-</b> 0.20	0.49	0.47	!			0.41	0.70				000
Verify score		-0.24	60.0	0.03	0.15	0.30				-0.10	0.57			,	7.
Psi Blast		4.5e-13	9.6e-15	4.8e-15	3e-13	1 10-07	) )			0.0003	6e-12				70000
END		261	349	450	265	293				49	293				Q,
STAR T AA		164	169	271	164	230	1			20	226				11
CHAI N ID		A	A	A		4				А	A				D
PDB ID		1qr4	1qr4	1qr4	1ttf	1412				1e0m	1ekz				1400
SEQ ID NO:		1894	1894	1894	1894	1895				1895	1895				180%

PDB annotation		PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13	
Coumpound		ISOMERASE NIMA- CHAIN; B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	MATERNAL EFFECT PROTEIN STAUFEN; 1STU 4	
Verify PMF SEQFOL	D score			
PMF	score		0.25	
	score		0.18	
Psi Blast			3e-05	
END	AA		293	
STAR	TAA		233	
PDB CHAI STAR	A Z			
PDB	<u> </u>		lstu	
SEQ	NO:		1895 1stu	

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
970	26	0.949	0.664
971	23	0.996	0.936
972	28	0.929	0.700
973	26	0.976	0.875
974	17	0.919	0.828
975	28	0.976	0.653
976	30	0.996	0.894
977	17	0.953	0.784
978	22	0.982	0.872
979	19	0.890	0.552
980	18	0.984	0.958
981	19	0.981	0.916
982	19	0.995	0.971
983	21	0.980	0.904
984	21	0.980	0.904
985	16	0.961	0.916
986	26	0.951	0.801
987	43	0.992	0.943
988	41	0.937	0.604
989	43	0.994	0.659
990	29	0.986	0.848
991	37	0.984	0.878
992	19	0.942	0.693
993	22	0.982	0.872
995	19	0.993	0.931
996	22	0.992	0.807
997	28	0.990	0.919
998	23	0.896	0.747
999	23	0.985	0.951
1000	21	0.989	0.925
1001	11	0.989	0.925
1001	18		0.634
1002	16	0.933 0.881	0.634

1005         18           1006         19           1007         24           1008         16           1009         31           1010         22           1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038	ino Acid SEquence	0.964 0.972 0.997 0.945 0.957 0.975 0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.812 0.915 0.929 0.737 0.775 0.822 0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703 0.749
1007         24           1008         16           1009         31           1010         22           1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040		0.997 0.945 0.957 0.975 0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.929 0.737 0.775 0.822 0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1008         16           1009         31           1010         22           1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041		0.945 0.957 0.975 0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.737 0.775 0.822 0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1009         31           1010         22           1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054		0.957 0.975 0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.775 0.822 0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1010         22           1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054         19           1055		0.975 0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.822 0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1011         28           1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.946 0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.799 0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1012         24           1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.973 0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.910 0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1013         29           1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.968 0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.769 0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1014         25           1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.977 0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.776 0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1015         41           1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1038         44           1039         29           1040         22           1041         29           1054         19           1056         25		0.986 0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.847 0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1016         28           1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.988 0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.938 0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1017         23           1018         45           1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.976 0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.897 0.657 0.604 0.776 0.679 0.594 0.925 0.703
1018       45         1019       28         1020       33         1021       18         1022       26         1023       31         1024       41         1025       36         1026       24         1027       27         1028       23         1029       22         1030       24         1031       34         1032       22         1033       25         1034       27         1035       19         1036       39         1037       28         1038       44         1039       29         1040       22         1041       29         1054       19         1055       16         1056       25		0.964 0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.657 0.604 0.776 0.679 0.594 0.925 0.703
1019         28           1020         33           1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.956 0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.604 0.776 0.679 0.594 0.925 0.703
1020       33         1021       18         1022       26         1023       31         1024       41         1025       36         1026       24         1027       27         1028       23         1029       22         1030       24         1031       34         1032       22         1033       25         1034       27         1035       19         1036       39         1037       28         1038       44         1039       29         1040       22         1041       29         1051       23         1054       19         1055       16         1056       25		0.948 0.930 0.947 0.991 0.942 0.910 0.988	0.776 0.679 0.594 0.925 0.703
1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.930 0.947 0.991 0.942 0.910 0.988	0.679 0.594 0.925 0.703
1021         18           1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1054         19           1055         16           1056         25		0.947 0.991 0.942 0.910 0.988	0.679 0.594 0.925 0.703
1022         26           1023         31           1024         41           1025         36           1026         24           1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1051         23           1054         19           1055         16           1056         25		0.947 0.991 0.942 0.910 0.988	0.594 0.925 0.703
1023       31         1024       41         1025       36         1026       24         1027       27         1028       23         1029       22         1030       24         1031       34         1032       22         1033       25         1034       27         1035       19         1036       39         1037       28         1038       44         1039       29         1040       22         1041       29         1054       19         1055       16         1056       25		0.942 0.910 0.988	0.925 0.703
1024     41       1025     36       1026     24       1027     27       1028     23       1029     22       1030     24       1031     34       1032     22       1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1055     16       1056     25		0.942 0.910 0.988	0.703
1025     36       1026     24       1027     27       1028     23       1029     22       1030     24       1031     34       1032     22       1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1055     16       1056     25		0.910 0.988	
1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1051         23           1054         19           1055         16           1056         25		0.988	0.749
1027         27           1028         23           1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1051         23           1054         19           1055         16           1056         25			0.919
1028       23         1029       22         1030       24         1031       34         1032       22         1033       25         1034       27         1035       19         1036       39         1037       28         1038       44         1039       29         1040       22         1041       29         1051       23         1054       19         1055       16         1056       25		0.962	0.696
1029         22           1030         24           1031         34           1032         22           1033         25           1034         27           1035         19           1036         39           1037         28           1038         44           1039         29           1040         22           1041         29           1051         23           1054         19           1055         16           1056         25		0.965	0.693
1030     24       1031     34       1032     22       1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.962	0.919
1031     34       1032     22       1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.943	0.832
1032     22       1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1055     16       1056     25		0.973	0.817
1033     25       1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.947	0.677
1034     27       1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.889	0.718
1035     19       1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.962	0.856
1036     39       1037     28       1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.967	0.909
1037     28       1038     44       1039     29       1040     22       1051     23       1054     19       1055     16       1056     25		0.986	0.922
1038     44       1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.982	0.924
1039     29       1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.974	0.662
1040     22       1041     29       1051     23       1054     19       1055     16       1056     25		0.984	0.763
1041     29       1051     23       1054     19       1055     16       1056     25		0.974	0.796
1051     23       1054     19       1055     16       1056     25		0.928	0.725
1054     19       1055     16       1056     25		0.966	0.812
1055         16           1056         25		0.951	0.895
1056 25		0.927	0.827
		0.949	0.823
1058 28		0.980	0.848
1061 24		0.965	0.891
1062 25		0.946	0.860
1067 36		0.964	0.648
1074 32		0.941	0.669
1076 17		0.995	0.974
1083 18		0.968	0.799
1089 24		0.882	0.599
1099 24		0.991	0.904
1091 38		0.991	0.888
1094 29 1096 19		U.70.3	
		0.800	0.715
1101 34		0.892	0.652 0.839
1102 20		0.921	11 7 2 13
1106     31       1110     36			0.659

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1174	18	0.975	0.958
1175	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197	15	0.977	0.966
1199	26	0.976	0.875
1200	28	0.973	0.822
1201	28	0.990	0.925
1205	22	0.982	0.933
1206	15	0.986	0.919
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226 1229	20	0.987	0.916
	30	0.996	0.894
1230 1234	41 20	0.203	0.791
		0.978	0.893
1239 1240	25	0.953	0.784
1241		0.974	0.897
1242	20		0.912
1247	35	0.974	0.817
1250 1251	22	0.982	0.872
			0.927
1254 1255	20	0.934 0.952	0.828
1256			0.807
	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	0.640
1263	33	0.953	0.707
1264	24	0.981	0.884
1265	24	0.987	0.914
1266	21	0.977	0.905

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1296	20	0.926	0.751
1302	29	0.981	0.937
1310	27	0.977	0.849
1314	24	0.977	0.845
1315	23	0.990	0.833
1317	25	0.971	0.894
1318	16	0.961	0.916
1319	41	0.980	0.681
1328	17	0.977	0.921
1329	26	0.993	0.894
1331	25	0.986	0.939
1333	33	0.977	0.811
1340	43	0.992	0.943
1341	20	0.943	0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	
			0.848
1369	18	0.997	0.979
1373	16	0.979	0.964
1375	25	0.980	0.952
1376	37	0.989	0.822
1378	37	0.984	0.878
1379	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.649
1467	41	0.990	0.922
1468	20	0.991	0.954
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	11	0.900	0.758
1493	18	0.933	0.634
1495	22	0.899	0.639
1496	40	0.953	0.668
1509	16	0.881	0.607
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	28	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	
			0.596
1600	29	0.968	0.769
1604	28	0.975	0.926
1613	25	0.977	0.776
1618	41	0.986	0.847
1627	24	0.915	0.578
1630	24	0.950	0.737
1631	28	0.987	0.785
1632	19	0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556
1684	18	0.930	0.679
1687	25	0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760	36	0.980	0.559
1769	10	0.880	0.780
1771	14	0.922	0.678
1773	39	0.982	0.829
1778	34	0.973	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
1826	36	0.951	0.782
1832	19	0.983	0.888
1833	23	0.971	0.941
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.942	0.737

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	44	0.974	0.662
1850	26	0.974	0.730
1851	27	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

## TABLE 7

SEQ ID	Chromsomal location
1	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21	2
22	11
23	12q
27	22q11
28	бр
29	6p23
31	17g
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10q26.2-10q26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52	19cen-q13.2
53	3p26

SEQ ID         Chromsomal location           54         2p24.3           55         3p26           56         3p26           57         15           60         15           62         1p21.2-22.3           65         11q12-q13.1           66         xp11           67         20q11.21-q13.12           69         2           70         X           71         1           72         1q21.2-q21.3           73         17p11.2           74         X           75         19           80         19           83         6q16           85         15           86         12           87         17q2-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19	
55         3p26           56         3p26           57         15           60         15           62         1p21.2-22.3           65         11q12-q13.1           66         xp11           67         20q11.21-q13.12           69         2           70         X           71         1           72         1q21.2-q21.3           73         17p1.2           74         X           75         19           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4	
56         3p26           57         15           60         15           62         1p21,2-22.3           65         11q12-q13.1           66         xp11           67         20q11,21-q13,12           69         2           70         X           71         1           72         1q21,2-q21,3           73         17p11,2           74         X           75         19           76         9           80         19           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32,3           94         14           95         7           96         10q26,1           97         9p21           98         16q24,3           99         5           101         15           102         19           103         6p21,3	
57     15       60     15       62     1p21.2-22.3       65     11q12-q13.1       66     xp11       67     20q11.21-q13.12       69     2       70     X       71     1       72     1q21.2-q21.3       73     17p11.2       74     X       75     19       76     9       80     19       83     6q16       85     15       86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3	
62         1p21.2-22.3           65         11q12-q13.1           66         xp11           67         20q11.21-q13.12           69         2           70         X           71         1           72         1q21.2-q21.3           73         17p1.2           74         X           75         19           76         9           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13	
65       11q12-q13.1         66       xp11         67       20q11.21-q13.12         69       2         70       X         71       1         72       1q21.2-q21.3         73       17p11.2         74       X         75       19         80       19         83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16	
65       11q12-q13.1         66       xp11         67       20q11.21-q13.12         69       2         70       X         71       1         72       1q21.2-q21.3         73       17p11.2         74       X         75       19         76       9         80       19         83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13	
66       xp11         67       20q11.21-q13.12         69       2         70       X         71       1         72       1q21.2-q21.3         73       17p11.2         74       X         75       19         76       9         80       19         83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16	
67       20q11.21-q13.12         69       2         70       X         71       1         72       1q21.2-q21.3         73       17p11.2         74       X         75       19         76       9         80       19         83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16         117       16	
69         2           70         X           71         1           72         1q21.2-q21.3           73         17p11.2           74         X           75         19           76         9           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13           112         9           114         2q35           115         22q13           116         16	
70         X           71         1           72         1q21.2-q21.3           73         17p11.2           74         X           75         19           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13           112         9           114         2q35           115         22q13           116         16           117         16           118         16q24.3	
71         1           72         1q21.2-q21.3           73         17p11.2           74         X           75         19           76         9           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13           112         9           114         2q35           115         22q13           116         16           117         16           118         16q24.3	
72         1q21.2-q21.3           73         17p11.2           74         X           75         19           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13           112         9           114         2q35           115         22q13           116         16           117         16           118         16q24.3           120         19	
73     17p11.2       74     X       75     19       80     19       83     6q16       85     15       86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
74         X           75         19           76         9           80         19           83         6q16           85         15           86         12           87         17q22-q24           88         8q22-q23           90         15           91         14q32.3           94         14           95         7           96         10q26.1           97         9p21           98         16q24.3           99         5           101         15           102         19           103         6p21.3           104         11p15.3-p15.4           105         16           107         14q32.1-q32.2           111         11q13           112         9           114         2q35           115         22q13           116         16           117         16           118         16q24.3           120         19	
75     19       76     9       80     19       83     6q16       85     15       86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
76       9         80       19         83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16         117       16         118       16q24.3         120       19	
80     19       83     6q16       85     15       86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
83       6q16         85       15         86       12         87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16         117       16         118       16q24.3         120       19	
85     15       86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
86     12       87     17q22-q24       88     8q22-q23       90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
87       17q22-q24         88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16         117       16         118       16q24.3         120       19	
88       8q22-q23         90       15         91       14q32.3         94       14         95       7         96       10q26.1         97       9p21         98       16q24.3         99       5         101       15         102       19         103       6p21.3         104       11p15.3-p15.4         105       16         107       14q32.1-q32.2         111       11q13         112       9         114       2q35         115       22q13         116       16         117       16         118       16q24.3         120       19	
90     15       91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
91     14q32.3       94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
94     14       95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	<del></del>
95     7       96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
96     10q26.1       97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
97     9p21       98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
98     16q24.3       99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
99     5       101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
101     15       102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
102     19       103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
103     6p21.3       104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
104     11p15.3-p15.4       105     16       107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
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107     14q32.1-q32.2       111     11q13       112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
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112     9       114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
114     2q35       115     22q13       116     16       117     16       118     16q24.3       120     19	
115     22q13       116     16       117     16       118     16q24.3       120     19	
116     16       117     16       118     16q24.3       120     19	
117     16       118     16q24.3       120     19	<del></del>
118     16q24.3       120     19	
120 19	
1.1	
123 20	
124 9	
125 3	
126 11	
127 22q11.2	
128 20q11.2-12	
129 14	
131 10q25.1	
133 17p11.2	
134 20	
136 4p16.3	

SEQ ID	Chromsomal location
137	12p13
138	19
139	1p34.1-p32
140	4 or 17
143	Xq13.1-13.3
144	3
145	3
146	5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167	6p21.3
168	16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	6p21.3
180	15q14
181	5q
183	5
184	11
187	11
188	3p21.3
189	12p13-qter
190	12p13-qter
191	12p13 qter
192	12p13 qter
193	2q34-q35
194	2q34-q35 2q34-q35
195	10
199	7q11-q22
200	7q11-q22
201	3
202	19q13.4
203	3
205	
206	Xq28
	6
208	Xq26.2-27.2
209	4
210	4
211	1q31
212	19q12-19q13.1
213	6q23

SEQ ID	Chromsomal location
214	10
215	1
216	1p32.2-34.2
217	8
218	11q13
219	1q21-q23
220	Xq28
221	16
222	17
223	1
224	19p13.3
225	19p11-q11
226	1
227	1
228	1
229	12
230	5
231	1p31
232	1p31.1-p22.3
233	22q11.23
234	22q12.1-q12.3
235	1
236	17
237	15
238	2p13
239	17
241	11p13
242	11
243	4q22-q24
244	12
245	19
246	5
247	14
248	16
249	14
250	4
251	19
252	9p22-p21_or_9p13
256	9p22-p21_0r_9p13
257	
	9q33-q34.1
258	12pter-p13.31
260	8
261	11q14
262	17
263	12q13
264	16q13-q21
265	16q13-q21
267	6q26-27
268	9q12-q21.2
269	9q12-q21.2
270	9q12-q21.2
271	19
272	1p34.1-35.3
273	11
274	11
275	X
277	2

SEQ ID	Chromsomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299	2p11
300	16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307	1p35-p34
308	9
309	16
310	21
311	12p13
312	1
313	1
314	17
315	1q42-q43
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320	6p21.32-22.1
321	6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324 325	6p21.32-22.1 6p21.32-22.1
326 327	3
328 332	14 17
335	17
336	14q32
337	
338	8q23
339	8q23
340	16q11.1-q11.2
341	8q22-q23
341	16p13.3
343	15
344	17
345	20q11.2-q13.1
346 347	20q11.2-q13.1
	19q13.3
348	19

SEQ ID	Chromsomal location
349	17q25.1
350	18
351	11
352	1
353	q25.1-31.1
354	11q14_
355	1q31
356	1q31
357	18
358	3p
359	10
360	7q22
361	7q22
362	1q21.3
363	3
364	18q12
365	11p15
367	14
369	1p36.21
371	6p12.3-21.1
373	14q13.1-14q21.3
374	15
375	4
376	7q32-q34
377	7q32-q34
378	20q13.1-q13.2
381	13
382	1q21.2-22
383	16
384	12
385	20q13.1
386	16
387	8q21.3-q22.1
388	11
389	15q22.1
390	17
391	17
394	8q23
395	15q24-q26
396	15q22
397	7q34-q36
399 400	2
401	6q21-22
	6q21-22
402	14q24.3
403 404	11-12
405	11q13
407	17
407	14
408	10
410	10q23-q24
411	19
	11
412 413	11p15
414	12q13.2-q13.3
414	3p13-q26.1
410	17

SEQ ID         Chromsomal location           421         5q35           422         3           423         12           424         3p24.3           425         19           426         6p21.1-21.2           427         6           428         22q13.2-q13.31           429         11           430         2           432         14q31           433         17           434         22           436         7q35           440         8p11.2           441         11q12           443         5           444         1           445         13q13           446         17           447         17           448         1p35.2-36.13           449         6           450         15q24-q25           451         19           452         4
422     3       423     12       424     3p24.3       425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
423     12       424     3p24.3       425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
424     3p24.3       425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
425     19       426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
426     6p21.1-21.2       427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
427     6       428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
428     22q13.2-q13.31       429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
429     11       430     2       432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
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432     14q31       433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
433     17       434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
434     22       436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
436     7q35       440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
440     8p11.2       441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
441     11q12       443     5       444     1       445     13q13       446     17       447     17       448     1p35,2-36,13       449     6       450     15q24-q25       451     19       452     4
443     5       444     1       445     13q13       446     17       447     17       448     1p35,2-36,13       449     6       450     15q24-q25       451     19       452     4
444     1       445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
445     13q13       446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
446     17       447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
447     17       448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
448     1p35.2-36.13       449     6       450     15q24-q25       451     19       452     4
449     6       450     15q24-q25       451     19       452     4
450     15q24-q25       451     19       452     4
451
452 4
453 2
454 11
455
456
457 p31.3-32.2
458 p51.3-52.2
459 7p13-p11.2
460 12
461 18p11.2
462 17
463 22q11.2
464 16
466 17
467 11q23
468 3
469 7q32
470 1
470 19
473 19
9p24.1-24.3
478 6p22.1-22.3
479 20
480 22q12.3-13.1
481 16q22.1-q22.3
483 19
484 19
489 6
491 1q21-q22

SEQ ID	Chromsomal location
492	4q26-q27
493	2p13
494	7
495	3
496	5
497	17q23.2-q25.3
498	liq
499	4p15.31
500	10
501	8q24.3
503	18
504	2
505	19
506	3p14.3
507	14
508	11p15,5
509	11
510	15q25
511	14q21.1-q22.3
512	13q11
513	10
514	Xq28
515	15q15
516	19p13.3
518	14q21
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519	13
520	12
521	12
522	20q12-q13.12
523	6q22.1-22.33
524	12
526	16
527	17
528	3
529	6p21.3
530	1q42.13-43
531	16p
532	17
533	16q24.1
534	19p13.3-p13.2
535	19p13.3-p13.2
536	13
537	17
538	12
539	1q21.2-q22
540	17
541	18q12
542	16
545	2p23.3-q34
546	14q21.1-q22.3
547	2p12
548	17q11-qter
549	4
550	17
551	9
552	17q24-q25

SEQ ID	Chromsomal location
553	12
554	5
555	17
556	10q23.3
557	9
558	9
559	X
560	20
562	16
563	15
564	3
565 566	4
567	6p22.1-23
568	<u>x</u> 5
570	19q13.4
572	1p36.23-p36.21
573	6
574	6p11.2-12.3
575	8
577	12
578	17
579	10
580	6p21
581	2
582	3q25.1-q25.2
583	3q25.1-q25.2
584	19
585	19p13.3
586	15
587	15
588	4q25
589	9p24
590	17
591	20q13.11-13.2
592	X
593 594	2p23.3-q24.3 6p22.1
595	1
596	1
597	2q31-q37
598	1p36.1
599	2p11.2-q11.2
600	19p13.1
601	2
602	17p13.3
603	15q
604	11
606	1p36
607	22q11.21
608	3
609	16
610	1
611	6
613	12
615	2p24.3
616	20q11.2

617 618 619 619 620 617 621 621 14 622 8 8 624 17 625 5 626 627 628 19 630 3p21.1-q13.13 631 20 632 20 634 636 636 637 2 638 639 8q22-q23 640 640 8 8 642 642 643 7 640 8 642 655 611 7 666 611 11 663 656 67 675 117 6666 666 677 676 676 679 18 676 676 679 18 676 677 678 686 677 678 676 677 678 676 677 678 676 677 678 676 677 677	SEQ ID	Chromsomal location
619         8q22           620         17q32.1           621         14           622         8           624         17           625         5           626         17           625         5           626         17q1           630         3p21.1-q13.13           631         20           632         20           634         6           637         2           638         20q13           639         8ç22-q23           640         8           642         5q21-q22           643         xq26           644         22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           3         3p13-q26.1           654         12q           655         12q           666         17           657         17	617	16
17q23.1   14   14   16   16   17   16   17   17   17   17		
621         14           622         8           624         17           625         5           626         17           628         19           629         17q11           630         3p21.1-q13.13           631         20           632         20           634         6           637         2           638         20q13           639         8022-q23           640         8           642         5q21-q22           643         x026           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           633         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11           663         6 <td< td=""><td>619</td><td>8q22</td></td<>	619	8q22
621         14           622         8           624         17           625         5           626         17           628         19           629         17q11           630         3p21.1-q13.13           631         20           632         20           634         6           637         2           638         20q13           639         8022-q23           640         8           642         5q21-q22           643         x026           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           633         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11           663         6 <td< td=""><td>620</td><td>17q23.1</td></td<>	620	17q23.1
624         17           625         5           626         17           628         19           629         17q11           630         3p21.1-q13.13           631         20           634         6           636         6           637         2           638         20q13           639         8u22-q23           640         8           642         5q21-q22           643         x026           644         22           643         x026           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11		14
625         5           626         17           628         19           629         17q11           630         3p21.1-q13.13           631         20           634         6           636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           646         2           647         2p23.3-q34           648         5           651         x           652         3           3p13-q26.1         12q           654         12q           655         12q           656         17           657         17           658         12           669         11           660         9q31           661         11           662         10	622	
17	624	17
628         19           629         17q11           630         3p21.1-q13.13           631         20           632         20           634         6           636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           643         11q25           644         22           647         2p23.3-q34           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           669         11           661         11           662         10           663         1           664         2p23.3-q24.3	625	
629         17q11           630         3p21.1-q13.13           631         20           632         20           634         6           636         6           637         2           638         20q13           639         8e22-q23           640         8           642         5q21-q22           643         11q25           644         22           643         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         12q           658         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3		
Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Signature   Sign	628	
631         20           632         20           634         6           636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           12q         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           669         11           670         21q22.3           671         4p16.1	629	17q11
632         20           634         6           636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11           662         10           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q2.3           671         4p16.1           672         11	630	3p21.1-q13.13
634         6           636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12	631	
636         6           637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19		
637         2           638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           679         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19	634	
638         20q13           639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q2.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25 <t< td=""><td></td><td>6</td></t<>		6
639       8q22-q23         640       8         642       5q21-q22         643       xq26         644       22         645       11q25         646       2         647       2p23.3-q34         648       5         651       X         652       3         653       3p13-q26.1         654       12q         655       12q         656       17         657       17         658       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5	637	
639         8q22-q23           640         8           642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25           678         5           679         x		20q13
642         5q21-q22           643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25           678         5           679         x           680         3p21.1-q12.3      <	639	8q22-q23
643         xq26           644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           655         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25           678         5           679         x           680         3p21.1-q12.3           681         5		
644         22           645         11q25           646         2           647         2p23.3-q34           648         5           651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           669         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25           678         5           679         x           680         3p21.1-q12.3           681         5	642	5q21-q22
645     11q25       646     2       647     2p23.3-q34       648     5       651     x       652     3       653     3p13-q26.1       654     12q       655     12q       656     17       657     17       658     12       659     12       660     9q31       661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       681     5       683     12p13.1-p12.3       684     17q		xq26
646       2         647       2p23.3-q34         648       5         651       x         652       3         653       3p13-q26.1         654       12q         655       12q         656       17         657       17         658       12         659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3	644	
647       2p23.3-q34         648       5         651       X         652       3         653       3p13-q26.1         654       12q         655       12q         656       17         657       17         658       12         659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	645	11q25
648       5         651       x         652       3         653       3p13-q26.1         654       12q         655       12q         656       17         657       17         658       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	646	2
651         x           652         3           653         3p13-q26.1           654         12q           655         12q           656         17           657         17           658         12           659         12           660         9q31           661         11           663         6           664         2p23.3-q24.3           666         10           667         21q           668         11           670         21q22.3           671         4p16.1           672         11           673         12           675         19           676         19           677         6p24-25           678         5           679         x           680         3p21.1-q12.3           681         5           683         12p13.1-p12.3           684         17q		2p23.3-q34
652     3       653     3p13-q26.1       654     12q       655     12q       656     17       657     17       658     12       659     12       660     9q31       661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	648	
653       3p13-q26.1         654       12q         655       12q         656       17         657       17         658       12         659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	651	X
654       12q         655       12q         656       17         657       17         658       12         659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	652	
655     12q       656     17       657     17       658     12       659     12       660     9q31       661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	653	3p13-q26.1
656       17         657       17         658       12         659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	654	
657     17       658     12       659     12       660     9q31       661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	655	
658     12       659     12       660     9q31       661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	656	
659       12         660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	657	
660       9q31         661       11         663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	658	
661     11       663     6       664     2p23.3-q24.3       666     10       667     21q       668     11       669     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	659	
663       6         664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q	660	
664       2p23.3-q24.3         666       10         667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q		11
666     10       667     21q       668     11       669     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
667       21q         668       11         669       11         670       21q22.3         671       4p16.1         672       11         673       12         675       19         676       19         677       6p24-25         678       5         679       x         680       3p21.1-q12.3         681       5         683       12p13.1-p12.3         684       17q		2p25.3-q24.3
668     11       669     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
669     11       670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		ZIQ
670     21q22.3       671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
671     4p16.1       672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
672     11       673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	6/0	
673     12       675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	6/1	
675     19       676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
676     19       677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
677     6p24-25       678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	6/3	19
678     5       679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
679     x       680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q	0//	op24-25
680     3p21.1-q12.3       681     5       683     12p13.1-p12.3       684     17q		
681     5       683     12p13.1-p12.3       684     17q		
683 12p13.1-p12.3 684 17q		
684 17q		

SEQ ID	Chromsomal location
685	19
686	19
687	19
688	19
689	7q31.1-q31.3
691	17
692	17
694	x
695	17
697	7p14.3-p14.1
698	5
699	18q12-q21
700	14q24.3
701	17
702	17
703	1
704	20p13
705	6pter-p21.1
706	17
708	8
711	1
712	2p24.3-p24.1
713	16
714	18q21
715	17
716	1932
717	1q32 1q12-21.1
718	18
720	17
721	11
722	11
723	15
724	5
726	7
727	17q21.3
728	11
729	5
730	12
731	4
731	
732	12
733	15q15
734	8q24.3
735	Xq26.3-27.3
736	19q13.2
737	21q22.1
738	5
740	13
742	1p36.2-p35
743	2
744	2
746	1
747	2q32-q33
748	2p23
749	13
750	4
751	17p11.2
752	1p13
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SEQ ID	Chromsomal location
753	5
754	11q13.1-q13.3
755	19
756	5pter-p13.3
757	10
758	19q13
760	19
761	14
762	19
763	X
765	X
766	9q34.3
767 769	17
769	5 14
770	14 17q12
772	20
773	17
774	8
775	3
776	15
777	8
778	6
779	17
780	15
781	14
782	11
783	19q13.4
784	8p11.2
785	8
786	8
787	17
788	8
789 790	1942.13-43
791	7q11.21-q11.23
792	3p13-q13.2
	9
794	11q12
795	1p32.2-34.2
797	18
	18
	11q13
	17
	7p15-p21
	17
	17p13.1
805	17q25.3
806	17q25
808	5
809	7p15-p14
	9q34.2-q34.3
	1
	6
	8
814	
	17 20

SEQ ID	Chromsomal location
816	7g34-g36
817	14q21.1-q21.3
818	1p32.1-33
819	5
820	6p21.3
821	17
822	15
823	5
824	19
825	1p32.3
826	11
827	14
828	p34.1-34.3
829	16
830	8p11.2
831	17q21.3-17q22
833	17
834	7p
835	21
836	10cen-q26.11
837	19 5
838	5
840	10
841	7q11-q22
842	11
843	17
844	3
845	17
846	17
847	17
848	10
849	6
850	5q
851	5
853	7q35-qter
854	19
855	19
857	8
858	16
860	10
861	19
863	18p11.2
864	17
866	15q15
867	7
868	12
869	1
870	11q23
871 872	16
	16p13.3
873	17q12-q21
874	11q13.5
875	11cen-q12.1
876 877	16q13 X
878	1q21-q23
879	xq22.1-q22.3

SEQ ID	Chromsomal location	
880	1p31.2-32.3	
881	19q13.3-q13.4	
883	3p	
884	7	
885	14q32	
886	2	
887	22q11.2	
888	12	
889	15	
890	18	
891	17	
892	Xq21.33-22.3	
893	6p21.32-22.2	
894	11	
895	7q33-q34	
897	13	
898	15	
901	15	
902	14	
904		
905	16p11.2	
	21q22.3	
907	10 X	
909		
910	10q26	
911	20	
912	1	
913	18	
914	6	
915	10	
916	13	
917	17	
919	15q15	
920	20	
921	22q12,3	
922	16	
923	11	
924	2q33.3	
927	9	
928	2q21	
929	19	
930	18	
931	16	
932	16	
934	11p15	
936	7q35	
937	6q22.1-22.33	
939	17	
940	17	
941	17	
942		
	4	
943	1p36.31-p36.11	
944	9	
945	12	
946	19p13.3	
947	22q11.2	
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TABLE 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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10	958	10
11	959	11
12	960	12
13	961	13
14	962	14
15	963	15
16	964	16
17	965	17
18	966	18
19	967	19
20	968	20
21	969	21
22	970	22
23	971	23
24	972	24
25	973	25
26	974	26
27	975	27
28	976	28
29	977	29
30	978	30
31	979	31
32	980	32
33	981	33
34	982	34
35	983	35
36	984	36
37	985	37
38	986	38
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40	988	40
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45	993	45
46	994	46
47	995	47
48	996	48
49	997	49
50	998	50
51	999	51
52	1000	52
53	1001	53
54	1002	54

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
55	1003	55
56	1004	56
57	1005	57
58	1006	58
59	1007	59
60	1008	60
61	1009	61
62	1010	62
63	1011	63
64	1012	64
65	1013	65
66	1014	66
67	1015	67
_68	1016	68
69	1017	69
70	1018	70
71	1019	71
72	1020	72
73	1021	73
74	1022	74
75	1023	75
76	1024	76
77	1025	77
78	1026	78
79	1027	79
80	1028	80
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82	1030	82
83	1031	83
84	1032	84
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86	1034	86
87	1035	87
88	1036	88
89	1037	89
90	1038	90
91	1039	91
92	1040	92
93	1041	93
94	1042	94
95	1043	95
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102	1050	102
103	1051	103
104	1052	104
105	1053	105
106	1054	106
107	1055	107
108	1056	108
109	1057	109
110	1058	110

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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112	1060	112
113	1061	113
114	1062	114
115	1063	115
116	1064	116
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122	1070	122
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124	1072	124
125	1073	125
126	1074	126
127	1075	127
128	1076	128
129	1077	129
130	1078	130
131	1079	131
132	1080	132
133	1081	133
134	1082	134
135	1083	135
136	1084	136
137	1085	137
138	1085	138
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140	1087	
141:	1089	140
142	1090	141
143	1090	
144	1092	143
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146	1094	146
147	1095	147
148	1096	148
149	1097	149
150	1098	150
151	1099	151
152	1100	152
153	1101	153
154	1102	154
155	1103	155
156	1104	156
157	1105	157
158	1106	158
159	1107	159
160	1108	160
161	1109	161
162	1110	162
163	1111	163
164	1112	164
165	1113	165
166	1114	166

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
167	1115	167
168	1116	168
169	1117	169
170	1118	170
171	1119	171
172	1120	172
173	1121	173
174	1122	174
175	1123	175
176	1124	176
177	1125	177
178	1126	178
179	1127	179
180	1128	180
181	1129	181
182	1130	182
183	1131	183
184	1132	184
185	1133	185
186	1134	186
187	1135	187
188	1136	188
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215	1163	214
216	1164	215
217	1165	
218	1166	217
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219	1167	219
220	1168	220
221	1169	221
222	1170	222

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
223	1171	223
224	1172	224
225	1173	225
226	1174	226
227	1175	227
228	1176	228
229	1177	229
230	1178	230
231	1179	231
232	1180	232
233	1181	233
234	1182	234
235	1183	235
236	1184	236
237	1185	237
238	1186	238
239	1187	239
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241	1189	241
242	1190	242
243	1191	243
244	1192	244
245	1193	245
246	1194	246
247	1195	247
248	1196	248
249	1197	249
250	1198	250
251	1199	251
252	1200	252
253	1201	253
254	1202	254
255	1203	255
256	1204	256
257	1205	257
258	1205	258
259	1207	259
260	1207	260
261	1209	261
262	1210	261
263	1210	263
264	1212	263
265	1213	
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266 267	1214	266
	1215	267
268	1216	268
269	1217	269
270	1218	270
271	1219	271
272	1220	272
273	1221	273
274	1222	274
275	1223	275
276	1224	276
277	1225	277
278	1226	278

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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280	1228	280
281	1229	281
282	1230	282
283	1231	283
284	1232	284
285	1233	285
286	1234	286
287	1235	287
288	1236	288
289	1237	289
290	1238	290
291	1239	291
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293	1241	293
294	1242	294
295	1243	295
296	1244	296
297	1245	297
298	1246	298
299	1247	299
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307	1255	307
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309	1257	309
310	1258	310
311	1259	311
312	1260	312
313	1261	313
314	1262	314
315	1263	315
316	1264	316
317	1265	317
318	1266	318
319	1267	319
320	1268	320
321	1269	320
322	1270	322
323	1271	323
324	1272	324
325	1273	325
326	1274	326
327	1275	327
328	1276	328
329	1277	329
330	1278	330
331	1279	331
332	1280	332
333	1281	333
334	1282	334

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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336	1284	336
337	1285	337
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339	1287	339
340	1288	340
341	1289	341
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343	1291	343
344	1292	344
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346	1294	346
347	1295	347
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349	1297	349
350	1298	350
351	1299	351
352	1300	352
353	1301	353
354	1302	354
355	1303	355
356	1304	356
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358	1306	358
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362	1310	362
363	1311	363
364	1312	364
365	1313	365
366	1314	366
367	1315	367
368	1316	368
369	1317	369
370	1318	370
371	1319	371
372	1320	372
373	1321	373
374	1322	374
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376	1324	376
377	1325	377
378	1326	378
379	1327	379
380	1328	380
381	1329	381
382	1330	382
383	1331	383
384	1332	384
385	1333	385
386	1334	386
387	1335	387
388	1336	
389	1337	388
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390	1338	390

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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393	1341	393
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395	1343	395
396	1344	396
397	1345	397
398	1346	398
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403	1351	403
404	1352	404
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406	1354	406
407	1355	407
408	1356	408
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410	1358	410
411	1359	411
412	1360	412
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414	1362	414
415	1363	415
416	1364	416
417	1365	417
418	1366	418
419	1367	419
420	1368	420
421	1369	421
422	1370	422
423	1371	423
424	1372	424
425	1373	425
426	1374	426
427	1375	427
428	1376	427
429	1377	429 430
430	1378	
431	1379	431
432	1380	432
433	1381	433
434	1382	434
435	1383	435
436	1384	436
437	1385	437
438	1386	438
439	1387	439
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441	1389	441
442	1390	442
443	1391	443
444	1392	444
445	1393	445
446	1394	446

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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448	1396	448
449	1397	449
450	1398	450
451	1399	451
452	1400	452
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454	1402	454
455	1403	455
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465	1413	465
466	1414	466
467	1415	467
468	1416	468
469	1417	469
470	1418	470
	1419	470
471 472	1420	
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473	1421	473
474	1422	474
475	1423	475
476	1424	476
477	1425	477
478	1426	478
479	1427	479
480	1428	480
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482	1430	482
483	1431	483
484	1432	484
485	1433	485
486	1434	486
487	1435	487
488	1436	488
489	1437	489
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492	1440	492
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494	1442	494
495	1443	495
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497	1445	497
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501	1449	501
502	1450	502

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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522	1470	522
523	1471	523
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557	1505	557
558	1506	558

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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561	1509	561
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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627	1575	627
628	1576	628
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633	1581	633
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664	1612	664
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667	1614	666
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670	1618	670

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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714	1662	714
715	1663	715
716	1664	716
717	1665	717
718	1666	718
719	1667	718
720	1668	720
721	1669	
		721
722	1670	722
723	1671	723
724	1672	724
725	1673	725
726	1674	726

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
727	1675	727
728	1676	728
729	1677	729
730	1678	730
731	1679	731
732	1680	732
733	1681	733
734	1682	734
735	1683	735
736	1684	736
737	1685	737
738	1686	738
739	1687	739
740	1688	740
741	1689	741
742	1690	742
743	1691	743
744	1692	744
745	1693	745
746	1694	746
747	1695	747
748	1696	748
749	1697	749
750	1698	750
751	1699	751
752	1700	752
753	1701	753
754	1702	754
755	1703	755
756	1704	756
757	1705	757
758	1706	758
759	1707	759
760	1708	760
761	1709	761
762	1710	762
763	1711	763
764	1712	764
765	1713	765
766	1714	766
767	1715	767
768	1716	768
769	1717	769
770	1718	770
771	1719	771
772	1720	772
773	1721	773
774	1722	774
775	1723	775
776	1724	776
777	1725	777
778	1726	778
779	1727	779
780	1728	780 781
781	1729	1 701

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
783	1731	783
784	1732	784
785	1733	785
786	1734	786
787	1735	787
788	1736	788
789	1737	789
790	1738	790
791	1739	791.
792	1740	192
793 794	1741	793
794	1742 1743	794
796	1744	795 796
797	1745	796
798	1746	798
799	1747	799
800	1748	800
801	1749	801
802	1750	802
803	1751	803
804	1752	804
805	1753	805
806	1754	806
807	1755	807
808	1756	808
809	1757	809
810	1758	810
811	1759	811
812	1760	812
813	1761	813
814	1762	814
815	1763	815
816	1764	816
817	1765	817
818	1766	818
819	1767	819
820	1768	820
821	1769	821
822	1770	822
823	1771	823
824	1772	824
825	1773	825
826	1774	826
827	1775	827
828	1776	828
829	1777	829
830	1778	830
831	1779	831
832	1780	832
833	1781	833
834	1782	834
835	1783	835
836	1784	836
837	1785	837
838	1786	838

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
839	1787	839
840	1788	840
841	1789	841
842	1790	842
843	1791	843
844	1792	844
845	1793	845
846	1794	846
847	1795	847
848	1796	848
849	1797	849
850	1798	850
851	1799	851
852	1800	852
853	1801	853
854	1802	854
855	1803	855
856	1804	856
857	1805	857
858	1806	858
859	1807	859
860 861	1808	860
	1809	861
862	1810	862
863	1811	863
864	1812	864
865	1813	865
866	1814	866
867	1815	867
868	1816	868
869	1817	869
870	1818	870
871	1819	871
872		. 872
873	1821	873
874	1822	874
875	1823	875
876	1824	876
877	1825	877
878	1826	878
879	1827	879
880	1828	880
881	1829	881
882	1830	882
883	1831	883
884	1832	884
885	1833	885
886	1834	886
887	1835	887
888	1836	888
889	1837	889
890	1838	890
891	1839	891
892	1840	892
893	1841	893
894	1842	894

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
895	1843	895
896	1844	896
897	1845	897
898	1846	898
899	1847	899
900	1848	900
901	1849	901
902	1850	902
903	1851	903
904	1852	904
905	1853	905
906	1854	906
907	1855	907
908	1856	908
909	1857	909
910	1858	910
911	1859	911
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913	1860	912
	1861	913
914	1862	914
915	1863	915
916	1864	916
917	1865	917
918	1866	918
919	1867	919
920	1868	920
921	1869 .	921
922	1870	922
923	1871	923
924	1872	924
925	1873	925
926	1874	926
927	1875	927
928	1876	928
929	1877	929
930	1878	930
931	1879	931
932	1880	932
933	1881	933
934	1882	934
935	1883	935
936	1884	936
937	1885	937
938	1886	938
939	1887	939
940	1888	940
941	1889	941
942	1890	942
943	1891	943
944	1892	944
945	1893	945
946	1894	946
947	1895	947
271	l	
948	1896	948

## **CLAIMS**

## WHAT IS CLAIMED IS:

5 1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 948, a mature protein coding portion of SEQ ID NO: 1 – 948, an active domain coding protein of SEQ ID NO: 1 – 948, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
  - 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

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- 4. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 5. A vector comprising the polynucleotide of claim 1.

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- 6. An expression vector comprising the polynucleotide of claim 1.
- 7. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 9. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949-1896).
  - 10. A composition comprising the polypeptide of claim 9 and a carrier.

11. An antibody directed against the polypeptide of claim 9.

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- 12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
  - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
  - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
  - 14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
    - 15. A method for detecting the polypeptide of claim 9 in a sample, comprising:
    - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
    - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.
- 16. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:
  - a) contacting the compound with the polypeptide of claim 9 under conditions sufficient to form a polypeptide/compound complex; and
  - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

- a) contacting the compound with the polypeptide of claim 9, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

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- 18. A method of producing the polypeptide of claim 9, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and
  - b) isolating the polypeptide from the cell culture or cells of step (a).
- 19. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.
  - 20. The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.

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- 21. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-948.
- 22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.

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23. The collection of claim 22, wherein the array detects full-matches to any one of the polynucleotides in the collection.

24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.

25. The collection of claim 21, wherein the collection is provided in a computer-readable format.

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- 26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.